

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2005, 01:11:00 ; Search time 6690 Seconds  
(without alignments)  
10748.511 Million cell updates/sec

Title: US-10-048-116-1  
Perfect score: 1484  
Sequence: 1 atgcggtgcagcagactct.....ttctccgcgactccgggtaa 1484

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_on.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484	100.0	1484	6 AX081280	AX081280 Sequence
2	956.6	64.5	1446	6 BD137962	BD137962 Monovalen
3	700.2	47.2	1045	6 C0806515	C0806515 Sequence
4	700.2	47.2	1108	6 C0806531	C0806531 Sequence
5	700.2	47.2	1108	6 C0806532	C0806532 Sequence
6	699.6	47.1	990	10 MMU294738	AJ294738 Mus muscu
7	699.6	47.1	1095	10 MMUG66	V00798 Mouse mRNA
8	699.6	47.1	1341	6 I07390	I07390 Sequence 4
9	699.6	47.1	1407	10 AF466698	AF466698 Mus muscu
10	699.6	47.1	1570	6 A22281	A22281 M.musculus
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12	699.6	47.1	1570	6 AR409372	AR409372 Sequence
13	699.6	47.1	1570	6 AR559698	AR559698 Sequence
14	699.6	47.1	1570	6 BD057272	BD057272 Gene enco
15	699.6	47.1	1570	10 AB097847	AB097847 Mus muscu
16	699	47.1	1158	6 AR160140	AR160140 Sequence
17	699	47.1	1188	6 AR160149	AR160149 Sequence
18	699	47.1	6729	6 AX080954	AX080954 Sequence
19	699	47.1	7528	6 AX080953	AX080953 Sequence

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26	696.4	46.9	1570	6 A77138	A77138 Sequence 6
27	695.4	46.9	1278	6 AR393789	AR393789 Sequence
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31	695	46.8	700	6 CQ806513	CQ806513 Sequence
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ALIGNMENTS

RESULT 1  
LOCUS AX081280 1484 bp DNA linear PAT 27-FEB-2001  
DEFINITION Sequence 1 from Patent WO0109194.  
ACCESSION AX081280  
VERSION AX081280.1 GI:13170129  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Glaichenhaus,N. and Malherbe,L.  
TITLE Recombinant proteins and molecular complexes derived therefrom, analogous to molecules involved in immune responses  
JOURNAL Patent: WO 0109194-A 1 08-FEB-2001;  
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)  
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ORIGIN

Query Match 100.0%; Score 1484; DB 6; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	CAGTCTCTCTGGAGACATTTGGCCAGTACACATGAATTTGATGTGATGAGTGTCTTCTAT	180
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Qy	121	CAGTCTCTCTGGAGACATTTGGCCAGTACACATGAATTTGATGTGATGAGTGTCTTCTAT	180
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Qy	181	GTGGACTTTGGATAAGAGAAACTGTCTGGAGGCTTCTGAGTTTGGCCAAATGTGATACTC	240
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Qy	241	TTTGAGCCCCAAGGTGAGTGCATAAANTAGCTGCAGAAAAACAACAATTTGGGAATCTTG	300
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Qy	241	TTTGAGCCCCAAGGTGAGTGCATAAANTAGCTGCAGAAAAACAACAATTTGGGAATCTTG	300
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Qy	301	ACTAAGAGGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTCCCC	360
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Qy	301	ACTAAGAGGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTCCCC	360
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Qy	361	AAGTCCCCTGTGCTGTGGGTCAGCCCAAACCCCTTATCTGCTTTGTGGACAACATCTTC	420
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Qy	421	CCACTGTGATCAACNTACATGCTCAGAAATAGCAAGTCAGTCA CAGACGGGTTTAT	480
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Qy	481	GAGACCACTTCTCGTCAACCGGTGAACATTCCTTCCACAGCTGTCTTATCTCACCTTC	540
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Qy	541	ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTTGGAGAGCGG	600
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Qy	601	GTTCTGAAACACTGGGAACCTGAGATTCACGCCCCCATGTGCAGAGCTGCAGAAAACTGGA	660
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Qy	661	GGTGGAGGATCCA CTACAGCTCCAATCAAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAG	720
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Qy	721	AAGGAAAATGCACAGCTGGAAATGGAGTTTGAAGCACTGGNAAAGGAACTGGGCTCAGGCA	780
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Qy	781	GCATCTGAGCCACAGAGGCCCAACATCAAGCCCTGTCTCTCATGCAATGCCAAGCACT	840
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Qy	901	ATCTCCCTGAGCCCCCATAGTACATGTGTGTGTGTGATGTGAGCGGAGGATGACCCAGAT	960
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Qy	961	GTCCAGATCAGCTGGTTTGTGAAACAAAGTGGAAAGTACACACAGCTCAGACACAAACCCAT	1020
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Qy	1021	AGAGAGGATTAACAAGTACTCTCTCCGGGTGTGAGTGGCCCTCCCATCTCAGACACAGGAC	1080
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QY	1081	TGGATGATGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGAGCTCCAGGCGCCCATC	1141		
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QY	1321	AACACTGAACGAGTCTCTGATGCTGATGGTTCTTACTTCAATGATACGAAGCTTGAGAGTG	1380		
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LOCUS	BD137962	1446 bp	DNA linear PAT 18-SEP-2002		
DEFINITION	Monovalent MHC-binding domain fused proteins and conjugates, polyvalent MHC-binding domain fused proteins and conjugates, polymer MHC-binding domain fused proteins and conjugates, and utilization therefor.				
ACCESSION	BD137962				
VERSION	BD137962.1	GI:23232907			
KEYWORDS	JP 2002504342-A/7.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 1446)				
AUTHORS	Wucherpfennig, K.W. and Strominger, J.L.				
TITLE	Monovalent MHC-binding domain fused proteins and conjugates, polyvalent MHC-binding domain fused proteins and conjugates, polymer MHC-binding domain fused proteins and conjugates, and utilization				
JOURNAL	Patent: JP 2002504342-A 7 12-FEB-2002; PRESIDENT AND FELLOWS OF HARVARD COLLEGE				
COMMENT	OS Artificial Sequence				
	PN JP 2002504342-A/7				
	PD 12-FEB-2002				
	PF 19-FEB-1999 JP 2000532537				
	PR 19-FEB-1998 US 60/075351				
	PI KAI W WUCHERPFENNIG, JACK L STROMINGER				
	PC C12N15/09,A61K35/14,A61K47/48,C07K14/705,C07K16/00,C07K19/00,				
	PC C12Q1/02,				
	PC G01N33/53,C12N15/00				
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	CC secretory signal				
	CC DRA*0101 extracellular domain				
	CC Linker				
	CC Fos leucine zipper domain				
	CC IgG domain				
	FH Key				
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ORIGIN
Query Match 64.5%; Score 956.6; DB 6; Length 1446;
Best Local Similarity 81.8%; Pred. No. 1.8e-251;
Matches 1135; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

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Qy 176 TCTATGTGGACTTGGATAAGAAAGAACTGCTCGAGGCTTCCTCGAGTTTGGCCAAATTGA 235
Db 110 TCCATGTGGATATGCCAAAGAGGAGCGGTCTGGCGCTTGAAGAAATTTGGACGATTTG 169

Qy 236 TACTCTTTGAGCCCAAGGTGGAATGCAAAACATAGCTGCGAAGAAACACAACTTTGGAA 295
Db 170 CCAGCTTTGAGGCTCAAGGTGCAATGGCCAAACATAGCTGTGGACAAAGCCCAACTTGGAA 229

Qy 296 TCTTGACTAGAGGTCAAAATTTACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGT 355
Db 230 TCATGACAAAGCGCTCCAACTATATCTCCGATCAACCAATGTACTCCAGAGTAACTGTGC 289

Qy 356 TCCCAAGTCCCTGTGCTGCTGGTCAAGCCCAACACCCCTTATCTGCTTTGTGACAACA 415
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Qy 416 TCTTCCCACTGTGATCAACATCATGGCTCAGAAATAGCAAGTCAAGTCAAGCGGCG 475
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Qy 476 TTTATGAGACAGCTTCTCTGCTCAACCGTGACCATCTCTTCCACAGCTGTCTTATCTCA 535
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Qy 536 CTTTCATCTCTCTGATGATCACAATTTATGACTCAAGGTGAGACACTGGGGCTGGAGG 595
Db 470 CTTCTCTGCTCTCACTGAGGACGTTTACGACTGAGGGTGGAGCACTGGGGCTTGGATG 529

Qy 596 AGCCGGTTCTGAAACACTGGGAACCTGAGATTCAGAGCCCCCATGTCAAGAGTGCAGAAA 655
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Qy 701 AAGAGCTCCAGGCCCTTGAGAGGAAATGACAGCTGGAATGGAGTTGCAAGCACTGG 760
Db 650 ACAGAAAGTCTGCTTGAGACCGAGATGTCGAATCTACTGAAGAGAGGAAAGAACTGG 709

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1478 CGGGTAA 1484
1430 CGGGTAA 1436

RESULT 3
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LOCUS Sequence 10 from Patent WO2004035622.
ACCESSION CQ806515
VERSION CQ806515.1 GI:47111911
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Dreher, I. and Moll, T.
TITLE Antagonists 11-15
JOURNAL Patent: WO 2004035622-A 10 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
Location/Qualifiers
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/note="DNA for fusionprotein"

ORIGIN
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Best Local Similarity 93.2%; Pred. No. 5.5e-181;
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy 760 GAAAGGAACCTGCGTCAAGCAGCATCTGAGCCAGAGGGCCCAACATCAAGCCCTGCTC 819
Db 316 ATGTGCAAAATGTTTCATCAACACTTTCGGATCCAGAGGGCCCAACATCAAGCCCTGCTC 375

Qy 820 CCATGCAAAATGCCAGACCTTAACCTTGGGTGGACCATCCGCTTTCATCTTCCCTCCA 879
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436 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCATAGTACATGTTGGTGGTGGAT 495
QY 940 GTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAAACAACGTTGGAATACAC 999
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496 GTGAGCGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAAACAACGTTGGAATACAC 555
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676 AAAGACCTCCAGACCCCATCGAGAGAACCATCTCAAAAACCCAAAGGTCAGTAAGAGCT 735
QY 1180 CCACAGGTATATGTTCTGCTCCACAGAGAGAGATGACTAAGAAACAGTCACTCTG 1239
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796 ACCTGCATGGTCAAGACTTTCATGCTGAAGACATTTACGTGGAGTGGACCAACACGG 855
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856 AAAACAGAGCTAAACTACAAGAACACTGAACCCAGTCTCGGACTCTGATGGTTCTTACTTC 915
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916 ATGTACAGAGCTGAGAGTGGAAGAGAACTGGGTGGAAAGAAATAGTACTCTCTGT 975
QY 1420 TCAGTGGTCCAGAGGGTCTGCACATCACCACAGCTTAAGAGCTTCTCCGGACTCCG 1479
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976 TCAGTGGTCCAGAGGGTCTGCACATCACCACAGCTTAAGAGCTTCTCCGGACTCCG 1535
QY 1480 GGTA 1484
Db |||||
1036 GGTA 1040

RESULT 4
CQ806531
LOCUS CQ806531 1108 bp DNA linear PAT 10-MAY-2004
DEFINITION Sequence 26 from Patent WO2004035622.
ACCESSION CQ806531
VERSION CQ806531.1 GI:47111925
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
1
AUTHORS Dreher, I. and Moll, T.
TITLE Antagonists il-15
JOURNAL Patent: WO 2004035622-A 26 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
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Best Local Similarity 93.2%; Pred. No. 5.5e-181;
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
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DEFINITION Sequence 27 from Patent WO2004035622.
ACCESSION CQ806532
VERSION CQ806532.1 GI:47111926
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
1
REFERENCE
1
AUTHORS Dreher, I. and Moll, T.
TITLE Antagonists il-15
JOURNAL Patent: WO 2004035622-A 27 29-APR-2004;
F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 47.2%; Score 700.2; DB 6; Length 1108;
Best Local Similarity 93.2%; Pred. No. 5.5e-181;
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 700 AAAGAGCTCCAGGCGCTGGAGAGGAAATGCACAGCTGGAGTGGAGTTCGAAGCACTG 759
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Qy 319 AAAGATGTGAGGAAGTGGAGGAAATATTAAGATTTTGGACAGTTTGTATCAT 378
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Db |||||
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RESULT 6
MMU294738 990 bp mRNA linear ROD 09-FEB-2001
LOCUS MMU294738
DEFINITION Mus musculus partial mRNA for immunoglobulin heavy chain constant
region gamma2a (IGHG2A gene).
ACCESSION AJ294738
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[illegible]

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RESULT 10
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LOCUS M.musculus OKT3 heavy chain. 1570 bp DNA linear PAT 09-JUL-2002
DEFINITION
ACCESSION A22261
VERSION A22261.1 GI:21727143
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE HUMANISED ANTIBODIES
JOURNAL Patent: WO 9109967-A 3 11-JUL-1991;
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        Query Match 47.1%; Score 699.6; DB 6; Length 1570;
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QY 906 CTTGAGCCCCATAGTACATGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA 965
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DB 925 GATCAGCTGTTTGTGAACAAGCTGGAGTACACACAGCTCAGACACAAACCCATAGAGA 984

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LOCUS AR029102 1570 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5859205.
ACCESSION AR029102
VERSION AR029102.1 GI:5941075
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1570)
AUTHORS Adair, J. Robert., Athwal, D. Singh. and Emtage, J. Spencer.
TITLE Humanised antibodies
JOURNAL Patent: US 5859205-A 6 12-JAN-1999;
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Qy	1446	TCACCAACAGCACTAAGAGCTTCTCCCGGAGCTCCGGGTAA	1484
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 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
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1570 bp mRNA  
 linear  
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 AR409372  
 AR409372  
 AR409372.1 GI:40160268  
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 Unknown.  
 Unknown.  
 Unclassified.  
 1 (bases 1 to 1570)  
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 Humanized antibodies  
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Qy	846	CTTGGGTGGACCAATCCGTCCTTCACTCTTCCCTCCAAAGATCAAGAGTACTCATGATCTC	905	
Db	805	CTTGGGTGGACCAATCCGTCCTTCACTCTTCCCTCCAAAGATCAAGAGTACTCATGATCTC	864	
Qy	906	CCTGAGCCCAATAGTCACATGTGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCA	965	
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Qy	1026	GGATTACAAAGTACTCTCCGGGTGGTCACTGGCCCTCCCATCCAGCACAGACTCGAT	1085	
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AR559698

LOCUS

DEFINITION

SEQUENCE

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

6 from patent US 6750325.

GI:53969764

Unknown.

Unclassified.

1 (bases 1 to 1570)

Jolliffe, L.K., Zivin, R.A., Adair, J.R. and Athwal, D.S.

CD3 specific recombinant antibody

Patent: US 6750325-A 6 15-JUN-2004;

Location/Qualifiers

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DNA

linear

PAT 08-OCT-2004

source

begin

Query Match	47.1%	Score 699.6	DB 6	Length 1570
Best Local Similarity	100.0%	Pred. No. 8.4e-181		
Matches 699	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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Qy	846	CTTGGGTGGACCATCCGTCTTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC	905	
Db	805	CTTGGGTGGACCATCCGTCTTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC	864	
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Qy	966	GATCAGCTGGTTTGTGAAACAAAGCTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA	1025	
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BD057272 1570 bp DNA linear PAT 27-AUG-2002
DEFINITION Gene encoding antimalathion monoclonal antibody.
ACCESSION BD057272
VERSION BD057272.1 GI:22602878
KEYWORDS JP 2001275682-A/9,
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1570)
AUTHORS Okawa,H., Nakata,M. and Yuasa,Y.
TITLE Patent: JP 2001275682-A 9 OCT-2001;
JOURNAL Patent: JP 2001275682-A/9
COMMENT KANKYO MEMEKI GIJUTSU KENKYUSYO KK
PN JP 2001275682-A/9
PD 09-OCT-2001
PF 31-MAR-2000 JP 2000098323
PI HIDEO OKAWA, MASANOBU NAKATA, YOJIRO YUASA
PC C12N15/09, C07K16/44, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/ PC
C12N15/02, C12P21/02, C12R1:19, C12N15/00,
PC C12P21/08// (C12N1/21, C12R1:19), (C12P21/02, C12R1:19), C12N15/00,
PC C12N5/00
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AB097847 1570 bp mRNA linear ROD 08-APR-2003
LOCUS Mus musculus mRNA for immunoglobulin gamma-2a heavy chain, complete
DEFINITION cds, anti-malathion monoclonal antibody MLT2-23.
ACCESSION AB097847
VERSION AB097847.1 GI:26665399
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K., Kawata,M. and Ohkawa,H. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Molecular characteristics of the monoclonal and recombinant antibodies specific to the insecticide malathion
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1570)
AUTHORS Nishi,K., Imajuku,Y., Nakata,M., Ohde,K., Miyake,S., Morimune,K., Kawata,M. and Ohkawa,H. Direct Submission
JOURNAL Submitted (11-DEC-2002) Kosuke Nishi, Kobe University, Research Center for Environmental Genomics, 1-1 Rokkodai-cho, Nada-ku, Kobe, Hyogo 657-8501, Japan (E-mail:nishikosuke@yahoo.co.jp, Tel:81-78-803-5863, Fax:81-78-871-3617)
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3'UTR

polyA\_site

ORIGIN

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Query Match 47.1%; Score 699.6; DB 10; Length 1570;  
Best Local Similarity 100.0%; Pred. No. 8.4e-181;  
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-10-048-116-1  
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1484	100.0	1484	5	AAF55098 DNA encod
2	1066.4	71.9	1676	4	AB199041 Murine pC
3	956.6	64.5	1446	2	AAT99707 DR2-IGG f
4	956.6	64.5	1446	2	AAX87813 HLA-DR2 a
5	725.2	48.9	2345	4	AB199027 IAS MBP 1
6	722.2	48.7	2343	4	AB199033 MBP 90-10
7	700.2	47.2	1045	12	ADO07566 Fusion pr
8	700.2	47.2	1108	12	ADO07578 Fusion pr
9	700.2	47.2	1108	12	ADO07577 Fusion pr
10	699.6	47.1	990	12	ADL15694 Murine im
11	699.6	47.1	1570	2	AAQ12637 Monoclonal
12	699.6	47.1	1570	12	ADQ91058 Murine OK
13	699.2	47.1	729	3	AAX35704 Human gly
14	699.2	47.1	1140	10	ADBE5817 Murine in
15	699	47.1	1158	2	AAT59350 1-153 del
16	699	47.1	1188	2	AAT59349 1-153 c-m
17	699	47.1	6729	4	AAF30341 Bicistron
18	699	47.1	7528	4	AAF30316 Bicistron
19	698	47.0	1341	1	AAN91659 Chimeric
20	698	47.0	1581	2	AAQ48037 Monoclonal

21	698	47.0	1645	2	AAQ54652 T84.12 He
22	697.4	47.0	1131	2	AAV55416 Chimeric
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24	697.4	47.0	1275	2	AAT62850 Mouse sol
25	696.4	46.9	699	3	AAX51300 Murine im
26	696.4	46.9	699	3	AAAS0055 Mouse imm
27	696.4	46.9	1707	3	AAZ35706 Human gly
28	696.2	46.9	1140	10	ADBE5819 Murine mu
29	695.4	46.9	1278	4	AAF76881 DNA encod
30	695.4	46.9	2709	4	AAF76889 Coding se
31	695	46.8	700	12	ADO07569 Fusion pr
32	693.2	46.7	1356	12	ADN97544 Artificia
33	693.2	46.7	1461	6	AAD22972 Mouse Zal
34	689.2	46.4	10512	4	AAAD09085 PUB115 pl
35	689.2	46.4	10512	6	AAK99698 DNA of pl
36	688.4	46.4	702	4	AAAD09045 Murine Im
37	688.4	46.4	702	6	AAK99695 Mouse IgG
38	687.4	46.3	777	12	ADQ31223 Cla88 II
39	682.8	46.0	1146	12	AD101041 Human/mur
40	681.6	45.9	1098	9	ACC43452 Nucleotid
41	681	45.9	1209	2	AAX34597 Murine IL
42	656.4	44.2	4713	2	AAV12067 Murine IA
43	650.4	43.8	2053	4	AB199029 IAS MBP 9
44	650.4	43.8	2059	4	AB199032 MBP 1-14
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ALIGNMENTS

RESULT 1  
AAF55098

ID AAF55098 standard; DNA; 1484 BP.

XX AAF55098;

AC AAF55098;

XX 15-MAY-2001 (first entry)

DT DNA encoding a fusion protein comprising an alpha chain of MHC.

DE Recombinant protein; alpha chain; beta chain; MHC; immunoglobulin;

XX major histocompatibility complex; Pc region; antigen; T lymphocyte;

XX immunostimulant; vaccine; infection; tumour; ss.

OS Synthetic.

XX Key Location/Qualifiers

PH CDS i. .1482

FT /\*tag= a

XX WO200109194-A1.

XX 08-FEB-2001.

PD 28-JUL-2000; 2000WO-FR002193.

XX 29-JUL-1999; 99FR-00009862.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Glaichenhaus N, Malherbe L;

XX WPI; 2001-182944/18.

XX P-PSDB; AAB67480.

XX New soluble recombinant protein, useful e.g. as immunostimulant,

XX comprises dimeric major histocompatibility complex molecule fused to

XX immunoglobulin Fc region.

XX Example 1; Page 31-33; 43pp; French.

XX The specification describes soluble recombinant proteins that comprise at

CC least a dimer formed from the alpha and beta-chains of MHC (major

CC histocompatibility complex) Class I and II molecules in which at least  
CC one chain has, attached to its C-terminus, at least part of the Fc region  
CC of an immunoglobulin. The recombinant proteins, when linked to an  
CC antigenic peptide, are used to count and/or purify antigen-reactive T  
CC lymphocytes and to characterize their phenotype, e.g. in preclinical  
CC evaluation of vaccines. They are also used as immunostimulants,  
CC particularly for vaccine development (against infections and tumours), to  
CC count and determine phenotype of autoreactive T cells in subjects with,  
CC or at risk of developing, autoimmune diseases, e.g. for staging or  
CC evaluating treatments, and (to purify and/or enrich Ag-reactive T cells  
CC from cell cultures or patient samples, for use in subsequent curative or  
CC preventative cellular therapy. The present sequence encodes a recombinant  
CC protein of the invention, comprising an alpha chain of MHC molecules  
XX  
SQ Sequence 1484 BP; 414 A; 394 C; 362 G; 314 T; 0 U; 0 Other;

Query Match 100.0%; Score 1484; DB 5; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 0;  
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Db	61	TGCGAGGTGAG	120
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QY	181	GTGAG	240
Db	181	GTGAG	240
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Db	241	TTTGAG	300
QY	301	ACTAAG	360
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QY	361	AAGTCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	420
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Db	721	AAGGAAATGCAAGCTGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA	780
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QY	1381	GAAGAAGAACTGGGTGGAAAGAAATAGTCTTCTGTTTCAAGTGTGTGTGTGTGTGTGTGT	1440
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QY	1441	CACATCACACACAGCTTACAGCTTCTCCCGGACTCCGGGTAA	1484
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## RESULT 2

ABI99041  
ID ABI99041 standard; cDNA; 1676 BP.

XX

AC ABI99041;

XX

DT 25-FEB-2002 (first entry)

XX

DE Murine pCB223 coding sequence.

XX 22-MAR-2000; 2000US-0191274P.  
PR 15-MAY-2000; 2000US-0204249P.  
PR 23-JAN-2001; 2001US-0264003P.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
PI Carter D, Zhu S, Arimilli S, Wang A;  
XX  
XX WPI; 2001-616371/71.  
XX P-PSDB; ABB56471.  
XX  
PT Multimeric complex for treating autoimmune diseases, comprises first and  
PT second single chain MHC class II molecules, each comprising alpha1 and  
PT beta1 domain linked through amino acid linker and multimerization domain.  
XX  
XX Disclosure; Page 115; 147pp; English.  
XX  
CC The invention relates to a multimeric complex comprising a first  
CC recombinant single chain major histocompatibility complex (MHC) class II  
CC molecule and a second recombinant single chain MHC class II molecule,  
CC each comprising an alpha1 domain and a beta1 domain linked through an  
CC amino acid linker and a multimerization domain. The first and the second  
CC molecule are linked through the multimerization domain to form a  
CC multimeric complex. The complex is useful for treating autoimmune  
CC diseases. It is useful for treating insulin dependent diabetes, multiple  
CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune  
CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus  
CC erythematosus. The present sequence encodes a single chain MHC class II  
CC molecule of the invention  
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Matches 1318; Conservative 0; Mismatches 96; Indels 164; Gaps 3;  
  
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Qy 127 CTTGGAGACATTGGCCAGTACACATGAATTTGATGTGTATGATGTTCTATGTGGAC 186  
Db 151 CTTGGAGACATTGGCCAGTACACATGAATTTGATGTGTATGATGTTCTATGTGGAC 210  
  
Qy 187 TTGATGAAGAGAACTGTCTGAGGCTTCTGAGTTCCTGAGTTTGGCCAACTGATCTTTGAG 246  
Db 211 TTGATGAAGAGAGAACTGTCTGAGTTCCTGAGTTCCTGAGTTTGGCCAACTGATCTTTGAG 270  
  
Qy 247 CCCCAAGGTGACGTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAG 306  
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Db 511 AGCTTCCTGTCACCCGTCACCAATTCCTTCCCAAGCTGTCTTATCTCACTTCATCCCT 570  
  
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Db 631 AAACACTGGGAACCTGAGATTTCAGCCGCCCATGTTCAGAGGATGTGCCAAAACACAGCC 690  
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Db 691 CCATCGGTCTATCCACTGGCCCTGTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTA 750  
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Qy 671 ----- 670  
Db 811 CTGTCCAGTGTGTGCACACCTTCCAGCTGTCTGTGAGTGTGACCTCTACACCTCAGC 870  
Qy 687 AGCTCAGCTGAAAGAGCTCCAGGCCCTGGAGAGGAAATGCACAGCTGGAAATGGGA 746  
Db 871 AGCTCAG--TGACTGTAACTCTGAGCACCTGGGCCAGCCAGTCCATCACCTGCAATGTGG 928  
Qy 747 GTTGAAGCACTGMAAAGAACTGGCTCAGGCGAGCATCTGAGCCAGAGGGCCCACAAT 806  
Db 929 CCACCCGCGCAGCAGCCAGGCTGAGCAAGAA--AATTGAGCCCAAGGGCCCACAAT 986  
Qy 807 CAAGCCCTGTCTCCATGCAAAATGCCAGCACCTTAACCTCTTGGGTGGACCATCCGCTTT 866  
Db 987 CAAGCCCTGTCTCCATGCAAAATGCCAGCACCTTAACCTCTTGGGTGGACCATCCGCTTT 1046  
Qy 867 CATCTTCCCTCAAAGATCAAGGATGTACTCATGTATCTCCTGAGCCCAATGATGACATG 926  
Db 1047 CATCTTCCCTCAAAGATCAAGGATGTACTCATGTATCTCCTGAGCCCAATGATGACATG 1106  
Qy 927 TGTGTTGTTGATGTGAGCGAGGATGACCCAGATGTCCAGATGATCAGCTGTTTGTGAACA 986  
Db 1107 TGTGTTGTTGATGTGAGCGAGGATGACCCAGATGTCCAGATGATCAGCTGTTTGTGAACA 1166  
Qy 987 CGTGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTTACAACAGTACTCTCCG 1046  
Db 1167 CGTGAAGTACACACAGCTCAGACACAAACCCATAGAGAGATTTACAACAGTACTCTCCG 1226  
Qy 1047 GGTGTTGAGTCCCTCCCATCAGACACAGGACTGATGAGTGGCAAGGATTTCAATG 1106  
Db 1227 GGTGTTGAGTCCCTCCCATCAGACACAGGACTGATGAGTGGCAAGGATTTCAATG 1286  
Qy 1107 CAAGGTCAACAAACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1166  
Db 1287 CAAGGTCAACAAACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGG 1346  
Qy 1167 GTCAAGTAAAGCTCCAGAGTATATGTCTTGGCTTCCACAGAGAGAGATGACTAAGAA 1226  
Db 1347 GTCAAGTAAAGCTCCAGAGTATATGTCTTGGCTTCCACAGAGAGAGATGACTAAGAA 1406  
Qy 1227 ACAGGTCACTCTGACCTGATGTGTCAAGCTTCTGATGCTGAGAGACATTTACGTGGAGT 1286  
Db 1407 ACAGGTCACTCTGACCTGATGTGTCAAGCTTCTGATGCTGAGAGACATTTACGTGGAGT 1466  
Qy 1287 GACCAACAGCGGAAACAGAGCTAACTACAGAACACCTGAAACCTGCTGGACTCTGA 1346  
Db 1467 GACCAACAGCGGAAACAGAGCTAACTACAGAACACCTGAAACCTGCTGGACTCTGA 1526  
Qy 1347 TGGTTCTTACTTCACTGATGACAGCAAGCTGAGAGTGGAAAGAGAACTGGGTGGAAAGAA 1406  
Db 1527 TGGTTCTTACTTCACTGATGACAGCAAGCTGAGAGTGGAAAGAGAACTGGGTGGAAAGAA 1586  
Qy 1407 TAGCTACTCTCTGTTTCAAGTGTGTGAGGGTGTGCACAATCAACACAGACTAAGAGCTT 1466  
Db 1587 TAGCTACTCTCTGTTTCAAGTGTGTGAGGGTGTGCACAATCAACACAGACTAAGAGCTT 1646  
Qy 1467 CTCCCGGACTCCGGGTAA 1484  
Db 1647 CTCCCGGACTCCGGGTAA 1664

RESULT 3  
 AAT99707  
 ID AAT99707 standard; cDNA; 1446 BP.  
 XX  
 AC AAT99707;  
 DT 17-OCT-2003 (revised)  
 DT 17-AUG-1998 (first entry)  
 XX  
 DE DR2-IgG fusion construct.  
 XX  
 KW Major histocompatibility complex class II; MHC class II; human; mouse;  
 KW fusion protein; HLA-DR2; DR2\*0101; binding domain; Fos;  
 KW dimerisation domain; IGG; allergy; autoimmune disease; vaccine;  
 KW multiple sclerosis; therapy; ss.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Chimeric.  
 XX  
 PN WO9806749-A2.  
 XX  
 PD 19-FEB-1998.  
 XX  
 PF 15-AUG-1997; 97WO-US014503.  
 XX  
 PR 16-AUG-1996; 96US-0024077P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Wucherpennig KW, Strominger JL;  
 XX  
 DR WPI; 1998-159459/14.  
 XX  
 PT New Class II MHC fusion proteins - comprising a MHC Class II binding  
 PT domain and a dimerisation domain or an immunoglobulin region used for  
 PT modulating immune responses.  
 XX  
 PS Example; Page 49; 76pp; English.  
 XX  
 CC This nucleotide sequences codes for a bivalent DR2 fusion protein  
 CC obtained by fusion of the Fc portion of IgG2a to the 3' end of a DR-alpha  
 CC -Fos cDNA construct (see AAV16866). The Fc portion was amplified by RT-  
 CC PCR from mouse hybridoma L243. The PCR product was then fused in frame  
 CC with the DR-alpha-Fos construct by overlapping PCR. The DR2-IgG fusion  
 CC was expressed in the Brosofilla Schneider cell system. The invention  
 CC relates to new soluble monovalent and multivalent Class II MHC fusion  
 CC proteins comprising a MHC Class II binding domain and a dimerisation  
 CC domain or an immunoglobulin region that can be used for the treatment of  
 CC allergic and autoimmune diseases (e.g. multiple sclerosis), for  
 CC tolerising a subject to foreign tissue before or after organ or tissue  
 CC transplantation, or for vaccination against pathogens. (Updated on 17-OCT  
 CC -2003 to standardise OS field)  
 XX  
 SQ Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;  
 Query Match 64.5%; Score 956.6; DB 2; Length 1446;  
 Best Local Similarity 81.8%; Pred. No. 1.8e-247;  
 Matches 1135; Conservative 0; Mismatches 234; Indels 18; Gaps 2;  
 QY 116 TTTATCAGTCTCTCGAGACATTGGCCAGTACACACATGAATTTTCATGGTATGATGTGT 175  
 DB 50 TCTATCTGAATCCTGACCATTGCGGAGTTTATGTTTGACTTTTATGGTATGATGATTT 109  
 QY 176 TCTATGTGGACTTGGATAAGAAAACTGTCTGGAGGCTTCTCGATTTGGCCAAATTGA 235  
 DB 110 TCCATGTGATATGCAAGAAGAGACGGTCTGCGGCTTGAAGATTTGGACATTG 169  
 QY 236 TACTCTTTGAGCCCAAGGTGACATGTCGAAAAACATAGCTGCGAAAAACAACTTTGGAA 295  
 DB 170 CCAGCTTTGAGGCTCAAGGTGCAATTTGGCCAAACATAGCTGTGACAAAGCCAACTTTGAAA 229  
 QY 296 TCTTGACTAAGAGGTCAAAATTTACCCCGAGCTACCAATGAGGCTCTCTCAGGCGATGTGT 355

Db TCATGACAAAGCGCTCCAACTATATCTCCGATCAACCAATGTACTCTCCAGAGTAACTGTGC 289  
 QY TCCCAAGTCCCTGT 415  
 Db TCAGAAACAGCCCTGT 349  
 QY TCTTCCGACCTGT 475  
 Db TCACCCCAACAGT 409  
 QY TTTATGAGACAGCTTCTCTGT 535  
 Db TGTGACAGACAGTCTTCTGT 469  
 QY CTTTCATCCCTTGT 595  
 Db CTTTCTGTCCCTCAACTGAGGACGTTTACGACTGCGGGTGGAGCACTGGGGCTTGGATG 529  
 QY AGCCGGTTCTGAAACACTGGGAACTGAGATTCAGCCCCCATGTGTGTGTGTGTGTGTGTGTGTGT 555  
 Db AGCCTCTTCTCAAGCACTGGGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589  
 QY CTGGAGGTGGAGGATCCACT-----ACAGCTCCATCAGCTCAGCTCGAAA 700  
 Db TCGACGGAGGTGGCGGGTTTAACTGATACACTCTCAAGCGGAGACAGATCAACTTGAAG 649  
 QY AAGAGCTCCAGGCCCTGTGAGAAAGAAATGACAGCTGGAATGGAGTTGCAAGCACTGG 760  
 Db ACGAGAGCTCTGCGTTGCGAGCCGAGATTGCCAATCTACTGAAAGAGAAAGAAAACCTGG 709  
 QY AAAAGGAACTG---GCTCAGGACAGCTGTGAGCCAGAGGGGCCCAACATCAAGCCCTGTC 817  
 Db AGTTCACTCTGCGCCGCCATCGACATCTGAGCCAGAGGGGCCCAACATCAAGCCCTGTC 769  
 QY CTCCATGCAAAATGCCAGCACCTAACTCTTGGGTGGACCACTCCGTCTTCACTTCCCTC 877  
 Db CTCCATGCAAAATGCCAGCACCTAACTCTTGGGTGGACCACTCCGTCTTCACTTCCCTC 829  
 QY CAAGATCAAGGATGTACTCATGTATCTCCCTGAGCCCATAGTCACTGTGTGTGTGTGTGTGTGT 937  
 Db CAAGATCAAGGATGTACTCATGTATCTCCCTGAGCCCATAGTCACTGTGTGTGTGTGTGTGTGT 889  
 QY ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 997  
 Db ATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 949  
 QY ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1057  
 Db ACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTG 1009  
 QY CCTTCCCATCCAGCACCGAGCTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 1117  
 Db CCTTCCCATCCAGCACCGAGCTGGATGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAT 1069  
 QY ACAAGAGCTCCAGCGCCCATCGAGAACCACTCTCAAAACCCCAAGGTCAGTAAGG 1177  
 Db ACAAGAGCTCCAGCGCCCATCGAGAACCACTCTCAAAACCCCAAGGTCAGTAAGG 1129  
 QY CTCACAGGATATGTCTTGTCTCCACAGAAAGAGATGACTAAGAAAAACAGGTCACCTC 1237  
 Db CTCACAGGATATGTCTTGTCTCCACAGAAAGAGATGACTAAGAAAAACAGGTCACCTC 1189  
 QY TGACCTGCATGGTCAAGACTTTCATGTGCTGAAGACATTTACGTGGAGTGGGACCAACAG 1297  
 Db TGACCTGCATGGTCAAGACTTTCATGTGCTGAAGACATTTACGTGGAGTGGGACCAACAG 1249  
 QY GAAAAACAGAGCTAAACTAGAAACACTGAAACAGTCTCTGACTCTGATGGTTCCTTACT 1357  
 Db GAAAAACAGAGCTAAACTAGAAACACTGAAACAGTCTCTGACTCTGATGGTTCCTTACT 1309  
 QY TCATGTACAGCAAGCTGAGAGTGGAAAAAGAACTGGGTGGAAAAAGAAATAGCTACTCTCT 1417



Db 1310 TCATGTACAGCACTGAGAGTGGAAAGAAAGAACTGGGTGGAAGAAATAGTACTCCT 1369

Qy 1418 GTTCAGTGGTCCAGAGGGTCTGCACAATCACACAGCACTTCTCCCGGACTC 1477

Db 1370 GTTCAGTGGTCCAGAGGGTCTGCACAATCACACAGCACTTCTCCCGGACTC 1429

Qy 1478 CGGGTAA 1484

Db 1430 CGGGTAA 1436

RESULT 4

AAX87813

ID AAX87813 standard; DNA; 1446 BP.

XX AC AAX87813;

XX AC

XX 09-NOV-1999 (first entry)

XX HLA-DR2 alpha-Fos-IgG fusion construct.

XX Major histocompatibility complex Class II; MHC; binding domain; HLA-DR2;

KW leucine zipper; Fos; IgG; Fc; immunoglobulin; antibody; fusion protein;

KW multiple sclerosis; rheumatoid arthritis; graft rejection; allergy;

KW autoimmune disease; pemphigus vulgaris; systemic lupus erythematosus;

KW T lymphocyte; T cell; diagnosis; therapy; adoptive immunotherapy; ss.

XX Homo sapiens.

OS Saccharomycetes cerevisiae.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT CDS 1..1440

FT /\*tag= a

FT sig\_peptide 1..15

FT /\*tag= b

FT /note= "alpha-mating factor secretion signal"

FT mat\_peptide 16..1437

FT /\*tag= c

FT /product= "DR2-Fos-Fc"

XX WO9942597-A1.

PN 26-AUG-1999.

XX 19-FEB-1999; 99WO-US003603.

PP 19-FEB-1998; 98US-0075351P.

XX (HARD ) HARVARD COLLEGE.

PA Wuchterpfennig KW, Strominger JL;

XX WPI; 1999-527481/44.

DR P-PSDB; AAY31654.

XX New HMC Class II binding domain fusion proteins and conjugates - used

PT for, e.g. treating allergic and autoimmune diseases or detecting,

PT isolating, activating or killing specific T cells.

XX Example 7; Page 100-102; 113pp; English.

XX This nucleotide sequence codes for a divalent HLA-DR2 MHC binding domain

CC fusion protein (see AAY31654) comprising an alpha-mating factor secretion

CC signal, the extracellular domain of the HLA-DR2 alpha chain (residues 1-

CC 191 of DRA\*0101), a 7-amino acid linker, the 40-amino acid leucine zipper

CC dimerization domain of Fos, and the Fc portion of IgG2a. The DR-alpha-Fc

CC chain corresponds to an antibody heavy chain. The invention provides new

CC monovalent, multivalent and multimeric MHC Class II binding domain fusion

CC proteins and conjugates comprising at least a binding domain of an MHC

CC Class II alpha or beta chain and a dimerization domain, especially a Fos

CC or Jun leucine zipper domain. The MHC fusion proteins and conjugates can

CC be used: for detecting and isolating T cells having a defined MHC/peptide

CC complex specificity (claimed); to confer to a subject adoptive immunity

CC to a defined MHC/peptide complex (claimed); to stimulate or activate T

CC cells reactive to a defined MHC/peptide complex (claimed); for selective

CC killing of T cells reactive to a defined MHC complex (claimed); to

CC tolerate a subject to a defined MHC/peptide complex (claimed); to treat

CC allergic and autoimmune diseases, e.g. multiple sclerosis, rheumatoid

CC arthritis, pemphigus vulgaris, and systemic lupus erythematosus; and to

CC prevent organ or tissue transplant rejection. The DR2-IgG design was

CC chosen to increase the affinity for the T cell receptor by increasing

CC valency, and to attach an effector domain, the Fc region of IgG2a.

CC Complement fixation may result in the lysis of target T cells following

CC binding of DR2-IgG molecules to the T cell receptor. DR2-IgG molecules

CC may therefore be useful for the selective depletion of autoaggressive T

CC cells

XX Sequence 1446 BP; 414 A; 375 C; 356 G; 301 T; 0 U; 0 Other;

SQ Query Match 64.5%; Score 956.6; DB 2; Length 1446;

Best Local Similarity 81.8%; Pred. No. 1.8e-247;

Matches 1135; Conservative 0; Mismatches 234; Indels 18; Gaps 2;

Qy 116 TTTATCAGTCTCCTGGAGACATTGGCCAGTACACACATGAATTTGATGGTGAAGTTGT 175

Db 50 TCTATCTGAATTCCTGACCAATCAGGGCGAGTTTATGTTTGACTTTTGATGGTGAAGTTT 109

Qy 176 TCTATGGAGCTTGGATAAGAAAGAAACTGCTGTGGAGGCTTCCTGAGTCTTGGCCAAATTGA 235

Db 110 TCCATGTGGATATGGCCAAAGAGAGACGGTCTGGCGGCTTGAAGAAATTTGGACGATTTG 169

Qy 236 TACTCTTTGAGCCCCCAAGTGGACTGCAAAACATAGCTGCAGAAAAAACAACAATTTGGAA 295

Db 170 CCAGCTTTTGAGGGCTCAAGGTGCATTGGCCAAACATAGCTGTGGCAAAAGCCAACTTGA 229

Qy 296 TCTTGACTAAGAGGTCAAATTTTACCCAGCTACCAATGAGGCTCTCAGCGGACTGTGT 355

Db 230 TCATGACAAAGCGCTCCAACTATCTCCGATCAACCAATGACTCCAGAGGTAATCTGTGC 289

Qy 356 TCCCCAAGTCCCTGTGCTGCTGGTGCAGCCCAACACCTTATCTGCTTTGTGACAACA 415

Db 290 TCAGGAACAGCCCTGTGGAACTGAGAGAGCCCAAGCTCTCATCTGTTTCATAGACAAGT 349

Qy 416 TCTTCCCACTGTGATCAACATCAGATGGCTCAGAAATAGCAAGTCACTCAGACAGCGCG 475

Db 350 TCACCCCAACAGTGGTCAATGTACAGTGGCTTCGAAATGAAACCTGTCAACACAGAG 409

Qy 476 TTTATGAGACAGCTTCTCTGTCACCGTGACCAATTCCTTCCACAACTGTCTTATCTCA 535

Db 410 TGTGAGACAGCTTCTCTGCTGCCAGGGAAGACCACCTTTTCCGCAAGTTCACATCTCC 469

Qy 536 CCTTTCATCCCTTCTGATGATGACATTTATGACTGCAAGTGGAGCACTGGGGCTGGAGG 595

Db 470 CCTTCTGCTCCCTCAACTGAGAGCGTTTACGACTGCAAGTGGAGCACTGGGGCTGGATG 529

Qy 596 AGCGGGTTCTGAAACACTGGGAACCTGAGATTCAGGCCCTCCATGTCAAGAGTGAAGAAA 655

Db 530 AGCTCTTCTCAAGCACTGGAGTTTGTATGCTCCAGCCCTCTCCCAAGAGACTACAGAGG 589

Qy 656 CTGGAGTGGAGGATCCACT-----ACAGCTCCATCAGCTCAGCTCGAAG 700

Db 590 TCGACGGAGGTGGCGCGGTTTAACTGATACACTCCAAAGCGGAGACAGATCAACTTGAAG 649

Qy 701 AAGAGCTCCAGGCCCTGGGAAGAAAGAAATGCAAGCTGGAATGGGAGTTCCAGCACTGG 760

Db 650 ACAGAAAGTCTGCGTTGACAGACCGAGATTCCTCAATCTACTGAAAGAGAAAGAAACTGG 709

Qy 761 AAAAGAAACTG---GCTCAGCGAGCACTCTGAGCCAGAGGGCCCAATCAAGCCCTGTGTC 817

Db 710 AGTTTCATCTGCGCGCCCATGACGATCTGAGCCAGAGGGCCCAATCAAGCCCTGTGTC 769

Qy 818 CTCATGCAAAATGCCAGACACCTAACTCTTTGGGTGACCATCGGTCTTATCTTCCTCCTC 877

Db 770 CTCATGCAAAATGCCAGACACCTAACTCTTTGGGTGACCATCGGTCTTATCTTCCTCCTC 829

QY 878 CAAAGATCAAGATGTAATCATGATCTCCCTGAGCCCATAGTACATGTGTGGTGG 937  
 Db 830 CAAAGATCAAGATGTAATCATGATCTCCCTGAGCCCATAGTACATGTGTGGTGG 889  
 QY 938 ATGTGAGCGAGATGATCACCAGATGTCAGATCAGCTGGTGTGTAACAACGTGGAAGTAC 997  
 Db 890 ATGTGAGCGAGATGATCACCAGATGTCAGATCAGCTGGTGTGTAACAACGTGGAAGTAC 949  
 QY 998 ACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCACTG 1057  
 Db 950 ACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCACTG 1009  
 QY 1058 CCTCCCATCCAGCACCAGACTGATGAGTGGCAAGAGTTCAAATGCAAGGTCAACA 1117  
 Db 1010 CCTCCCATCCAGCACCAGACTGATGAGTGGCAAGAGTTCAAATGCAAGGTCAACA 1069  
 QY 1118 ACAAGAGCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGAG 1177  
 Db 1070 ACAAGAGCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGAG 1129  
 QY 1178 TTCCACAGGTATATGCTTGTGCTCCACAGAGAGAGATGACTAAGAAACAGGTCACTC 1237  
 Db 1130 TTCCACAGGTATATGCTTGTGCTCCACAGAGAGAGATGACTAAGAAACAGGTCACTC 1189  
 QY 1238 TGACCTGATGTCAGACTTCATGCTGCTGAGAGATTTACGAGTGGACCAACAG 1297  
 Db 1190 TGACCTGATGTCAGACTTCATGCTGCTGAGAGATTTACGAGTGGACCAACAG 1249  
 QY 1298 GGAAACAGAGCTTAACTACAGAACACACTGGAACCACTCTGAGCTCTGATGTTCTTACT 1357  
 Db 1250 GGAAACAGAGCTTAACTACAGAACACACTGGAACCACTCTGAGCTCTGATGTTCTTACT 1309  
 QY 1358 TCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCT 1417  
 Db 1310 TCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCT 1369  
 QY 1418 GTTCAGTGGTCCAGAGGCTGCAATCACCACCAAGTAAAGCTTCTCCCGGACTC 1477  
 Db 1370 GTTCAGTGGTCCAGAGGCTGCAATCACCACCAAGTAAAGCTTCTCCCGGACTC 1429  
 QY 1478 CGGGTAA 1484  
 Db 1430 CGGGTAA 1436  
 RESULT 5  
 ABI99027  
 ID ABI99027 standard; cDNA; 2346 BP.  
 XX  
 AC ABI99027;  
 XX  
 DT 25-FEB-2002 (first entry)  
 XX  
 DE IAS MBP 1-14 CH1.CH2.CH3 coding sequence.  
 XX  
 KW Mouse; MHC; major histocompatibility complex; MHC class II; multimer;  
 single chain; immunosuppressive; antidiabetic; antiinflammatory;  
 KW antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;  
 KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;  
 KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;  
 KW rheumatoid arthritis; systemic lupus erythematosus; ss.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 PN WO200170245-A1.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 22-MAR-2001; 2001WO-US009616.  
 XX  
 PR 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.  
 PR 23-JAN-2001; 2001US-0264003P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Carter D, Zhu S, Arimilli S, Wang A;  
 XX  
 PI WPI; 2001-616371/71.  
 DR P-PSDB; ABB56457.  
 XX  
 PT Multimeric complex for treating autoimmune diseases, comprises first and  
 second single chain MHC class II molecules, each comprising alpha and  
 beta domain linked through amino acid linker and multimerization domain.  
 PT  
 XX  
 PS Disclosure; Page 91-92; 147pp; English.  
 XX  
 CC The invention relates to a multimeric complex comprising a first  
 recombinant single chain major histocompatibility complex (MHC) class II  
 molecule and a second recombinant single chain MHC class II molecule,  
 CC each comprising an alpha domain and a beta domain linked through an  
 amino acid linker and a multimerization domain. The first and the second  
 CC molecule are linked through the multimerization domain to form a  
 CC multimeric complex. The complex is useful for treating autoimmune  
 CC diseases. It is useful for treating insulin dependent diabetes, multiple  
 CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune  
 CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus  
 CC erythematosus. The present sequence encodes a single chain MHC class II  
 CC molecule of the invention  
 XX  
 SQ Sequence 2346 BP; 560 A; 663 C; 646 G; 477 T; 0 U; 0 Other;  
 Query Match 48.9%; Score 725.2; DB 4; Length 2346;  
 Best Local Similarity 70.5%; Pred. No. 6.3e-185;  
 Matches 1094; Conservative 0; Mismatches 323; Indels 135; Gaps 4;  
 QY 68 GTGAGAGCAGCATTTGAGGCCGACCCAGCAGTGTCTTATGTGTACAACTCTTATCAGTCTC 127  
 Db 779 GTGAGAGCAGCATTTGAGGCCGACCCAGCAGTGTCTTATGTGTACAACTCTTATCAGTCTC 838  
 QY 128 CTGAGAGCATTTGGCCAGTACACATGAATTTGATGTGATGAGTTGTTCTATGTGGACT 187  
 Db 839 CTGAGAGCATTTGGCCAGTACACATGAATTTGATGTGATGAGTTGTTCTATGTGGACT 898  
 QY 188 TGGATAGAGAAACATCTCTGGAGGCTTCTGAGTTTGGCCAAATTGATCTCTTTGAGC 247  
 Db 899 TGGATAGAGAGGAGCATATCTGAGTGTCTTCTGAGTTTGGCCAAATTGACAACTTTGACC 958  
 QY 248 CCCAAGTGGAGTGCAGAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGA 307  
 Db 959 CCCAAGTGGAGTGCAGAAACATAGCTGCAGAAAAACATAGCTTGGGAATCTTGACTAAGA 1018  
 QY 308 GGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCAGCTGTGTGTTCCCAAGTCCC 367  
 Db 1019 GGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCAGCTGTGTGTTCCCAAGTCCC 1078  
 QY 368 CTGTGCTGCTGGTCCAGCCCAACCCCTTATCTGCTTTGTGTGACAAACATCTTCCACCTG 427  
 Db 1079 CTGTGCTGCTGGTCCAGCCCAACCCCTTATCTGCTTTGTGTGACAAACATCTTCCCTCTG 1138  
 QY 428 TGATCAACATCAGATGGCTCAGAAATAGCAAGTGTGATCAGAGCGGCTTTATGAGACCA 487  
 Db 1139 TGATCAACATCAGATGGCTCAGAAATAGCAAGTGTGATCAGAGCGGCTTTATGAGACCA 1198  
 QY 488 GCTTCTCTCGTCAACCGTGAACCATTCCTTTCCAAAGCTGTCTTATCTACCTTCACTCCCTT 547  
 Db 1199 GCTTCTCTCGTCAACCGTGAACCATTCCTTTCCAAAGCTGTCTTATCTACCTTCACTCCCTT 1258  
 QY 548 CTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGGTTCTGA 607  
 Db 1259 CTGATGATGATTTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGGTTCTGA 1318  
 QY 608 AACACTGGG-----AA 618  
 |||||

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Db 1319 AACACTGGGTAGCGGAGGGGGCGGAAGCGCGGAGGGGGAGCCAAAGACACCCCCAT 1378
Qy 619 CCTGAGATTCAGGCCCCCATGTCAGAGCTGACAGAA----- 654
Db 1379 CTGTCATTCACACTGGCCCTGGATCTGTCGCCAACTAACTCCATGGTGACCTGGAT 1438
Qy 655 -ACTGGAGTGGAGATCCACTACAGTCCATCAGTCCAGTCCGAAAGAGCTCCAGGC 713
Db 1439 GCCTGGTCAAGGGCTATTTCCTGAGCCAGTGACAGTCCAGTCCGATCCCTGT 1498
Qy 714 CCTGGAGAAGGAAAT-----GACAG 735
Db 1499 CCAGCGTGTGCACACCTTCCAGCTGTCGAGTCTGACCTTACACTGTGAGCAGCT 1558
Qy 736 CTGGAATGGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCAGCATCTGAGCCGAGA 795
Db 1559 CAGTGACTGTCCCTCCAGCACCTGGCCGAGAGACCGTCACCTGCAACGTTGCCACC 1618
Qy 796 GGGCCCAATCAAGCCCTGTCTCTCATGCAATGCCCAG----- 835
Db 1619 CGGCCAGCAGCACCAAGGTGGACAAGAAATTTGTGCCCAGGGATTGTGTTGAAGCCTT 1678
Qy 836 ---CACCTAACCTCTTGSETGGACCATCCGTCCTTCACTCTCCCTCCAAAGATCAAGGATG 892
Db 1679 GCATATGTACAGTCCCAAGATATCATCTGTCTTCATCTTCCCCCAGGAGCCCAAGGATG 1738
Qy 893 TACTCATGATCTCCCTGAGCCCATAGTCAATGTGTGGTGGATGTGAGCGAGGATG 952
Db 1739 TGCTCACCATTACTCTGACTCTAAAGGTCAAGTGTGTGTGTAGATCATCAGCAAGGATG 1798
Qy 953 ACCAGATGTCAGATCAGCTGGTTGTGAAACAAGCTGGGAAGTACACAGCTCAGACAC 1012
Db 1799 ATCCGAGGTCCAGTTCAGCTGGTTGTGTAGATGATGTGGAGTGCACACAGCTCAGACGC 1858
Qy 1013 ARAACCATAGAGAGATTACAACGATCTCCGGGTGTTCAGTCCCTCCCATCCAGC 1072
Db 1859 AACCCTGGAGGAGCAGTCAACAGCACCTTTCGCTCAGTCAGTGAACCTTCCCCATATGC 1918
Qy 1073 ACCAGGACTGATGAGTGGCAAGGAGTCAAAATCAAGGTCAACACAAAGACCTCCAG 1132
Db 1919 ACCAGGACTGGCTCAATGGCAAGGAGTCAAAATCAGGTTCAACAGGTGCGAGCTTCCCTG 1978
Qy 1133 CGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAAGAGTCCACAGGTATATG 1192
Db 1979 CCCCCATCGAAGAAACCATCTCCAAACCCAAAGGCGACGAGGCTCCACAGGTGACA 2038
Qy 1193 TCTTGCTCCACAGAGAAGAGATGACTAAGAAAGGTCACTCTGACCTGCATGTCA 1252
Db 2039 CCATTCCACCTCCCAAGGAGCAGATGGCCCAAGGATNAAGTCAGTCTGACCTGCATGATA 2098
Qy 1253 CAGACTTCATGCGCTGAAGACATTTACGTGGAGTGGACCAACACGCGGAAACAGAGCTAA 1312
Db 2099 CAGACTTCTTCCCTGAAGACATTTACTGTGAGTGGCAGTGGATGGCAGCGGAGA 2158
Qy 1313 ACTACAAGAACACTGAACCGAGTCTCGACTCTGATGTTCTTACTTCATGTACAGCAAGC 1372
Db 2159 ACTACAAGAACACTCAGCCCATCATGTGACACAGATGCTTCTTACTCTGTACAGCAAGC 2218
Qy 1373 TGAGAGTGGAAAGAGAAGACTGGGTGGAAAGAAATAGTACTCTCTGTTCAGTGTCCAG 1432
Db 2219 TCAATGTGCAAGAGAGCAACTGGGAGGACAGAAATATCTTTCACTGTCTGTGTACATG 2278
Qy 1433 AGGCTCTGCAAAATCACACACGACTAAGAGCTTCTCCCGAGCTCCGGGTAA 1484
Db 2279 AGGCTCTGCAAAACCAACCATCTAGAGAGAGGCTCTCCCACTCTCTCTGGTAA 2330
```

## RESULT 6

ABI99033

ID ABI99033 standard; cDNA; 2343 BP.

XX

AC ABI99033;

XX

25-FEB-2002 (first entry)

MBP 90-101 CH1.H.CH2.CH3 coding sequence.

Mouse; MHC; major histocompatibility complex; MHC class II; multimer;  
single chain; immunosuppressive; antidiabetic; antiinflammatory;  
antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;  
autoimmune disease; insulin dependent diabetes; multiple sclerosis;  
myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;  
rheumatoid arthritis; systemic lupus erythematosus; ss.

Mus sp.

Synthetic.

WO200170245-A1.

27-SEP-2001.

22-MAR-2001; 2001WO-US009616.

22-MAR-2000; 2000US-0191274P.

15-MAY-2000; 2000US-0204249P.

23-JAN-2001; 2001US-0264003P.

(CORI-) CORIXA CORP.

Carter D, Zhu S, Arimilli S, Wang A;

WPI; 2001-616371/71.

P-PSDB; ABB56463.

Multimeric complex for treating autoimmune diseases, comprises first and  
second single chain MHC class II molecules, each comprising alpha and  
beta domain linked through amino acid linker and multimerization domain.

Disclosure; Page 96; 147pp; English.

The invention relates to a multimeric complex comprising a first  
recombinant single chain major histocompatibility complex (MHC) class II  
molecule and a second recombinant single chain MHC class II molecule,  
each comprising an alpha domain and a beta domain linked through an  
amino acid linker and a multimerization domain. The first and the second  
molecule are linked through the multimerization domain to form a  
multimeric complex. The complex is useful for treating autoimmune  
diseases. It is useful for treating insulin dependent diabetes, multiple  
sclerosis, myasthenia gravis, pernicious anaemia, autoimmune  
encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus  
erythematosus. The present sequence encodes a single chain MHC class II  
molecule of the invention

Sequence 2343 BP; 562 A; 665 C; 635 G; 481 T; 0 U; 0 Other;

Query Match 48.7%; Score 722.2; DB 4; Length 2343;  
Best Local Similarity 70.4%; Pred. No. 4.1e-184;  
Matches 1094; Conservative 0; Mismatches 323; Indels 138; Gaps 4;

Qy 68 GTCAAGACGACATTTGAGCGCGACACGCTAGCTTCTATGTGTACAACTGTTTATCAGTCTC 127  
Db 773 GTGAAGACGACATTTGAGCGCGACACGCTAGCTTCTATGTGTACAACTGTTTATCAGTCTC 832  
Qy 128 CTGGAGACATTTGCGCCAGTACACATGAAATTTGATGGTATGATGTTCTTATGTGAGCT 187  
Db 833 CTGGAGACATTTGCGCCAGTACACATGAAATTTGATGGTATGATGTTCTTATGTGAGCT 892  
Qy 188 TGATTAAGAGAAACATGTTCTGGAGGTTCTGAGTTGGCCCAATTGATCTTTTGGAGC 247  
Db 893 TGGTAAGAGAGGAGACTATCTGGATGCTTCTCGAGTTTGGCCCAATTGACAGCTTTTGACC 952  
Qy 248 CCCAAGGTGGACTGCAAAACATAGCTGCAGAAAACAACTTGGGAATCTTGACTAAGA 307  
Db 953 CCCAAGGTGGACTGCAAAACATAGCTGCAGAAAACAACTTGGGAATCTTGACTAAGA 1012  
Qy 308 GGTCAAAATTTTCCAGCCAGCTACCAATGAGGCTCTCTCAAGCGGAGTGTGTTCCCCAAGTCCC 367





QY 1060 CTCCCATCCAGCACCAGGACTGGATGAGTGGCAGAGGATTCAATGCAAGGTCAACAA 1119  
Db 679 CTCCCATCCAGCACCAGGACTGGATGAGTGGCAGAGGATTCAATGCAAGGTCAACAA 738  
QY 1120 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 1179  
Db 739 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 798  
QY 1180 CCACAGGTATATGTCTTGCTCCACCGAAGAGAGATGACTAAGAAACAGGTCACTCTG 1239  
Db 799 CCACAGGTATATGTCTTGCTCCACCGAAGAGAGATGACTAAGAAACAGGTCACTCTG 858  
QY 1240 ACCTGCATGGTCACAGACTTCATGCTGCAAGACATTTAGTGGAGTGACCAACACGG 1299  
Db 859 ACCTGCATGGTCACAGACTTCATGCTGCAAGACATTTAGTGGAGTGACCAACACGG 918  
QY 1300 AAAACAGAGCTAAATCTACAAGAACTGAACAGCTCTGGACTCTGATGGTCTTACTTC 1359  
Db 919 AAAACAGAGCTAAATCTACAAGAACTGAACAGCTCTGGACTCTGATGGTCTTACTTC 978  
QY 1360 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTCTCTGT 1419  
Db 979 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTCTCTGT 1038  
QY 1420 TCAGTGGTCCAGAGGGTCTGCAGAACTACACACAGACTTAAGAGCTTCTCCGGACTCG 1479  
Db 1039 TCAGTGGTCCAGAGGGTCTGCAGAACTACACACAGACTTAAGAGCTTCTCCGGACTCG 1098  
QY 1480 GGTA 1484  
Db 1099 GGTA 1103

## RESULT 9

ADO07577  
ID ADO07577 standard; DNA; 1108 BP.  
XX ADO07577;  
AC ADO07577;  
DT 15-JUL-2004 (first entry)  
XX Fusion protein coding sequence fragment Igk8.  
DE immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
KW neuroprotective; antipsoriatic; dermatological; antiinflammatory;  
KW cytostatic; interleukin-15; immunoglobulin G; ds; gene.  
XX Synthetic.  
OS Unidentified.  
XX WO2004035622-A2.  
PN 29-APR-2004.  
PD 13-OCT-2003; 2003WO-CH000666.  
XX 14-OCT-2002; 2002EP-00022869.  
PR (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
PA Dreher I, Moll T;  
XX WPI; 2004-357203/33.  
DR New fusion protein of interleukin-15 and Fc fragment, useful for treating  
PT e.g. transplantation disorders, autoimmune diseases and tumors, also  
PT related nucleic acid.  
XX Disclosure; Fig 10; 63pp; German.  
PS The present invention relates to a fusion protein consisting of wild-type  
CC interleukin-15 (IL-15) and an immunoglobulin G (IgG) Fc fragment, other

CC than a murine IgG2b Fc fragment. The fusion proteins and coding sequences  
CC are used to prevent or treat consequences of transplantation and/or  
CC autoimmune diseases, e.g. rheumatoid arthritis, diabetes, multiple  
CC sclerosis, psoriasis, neurodermatitis, ulcerative colitis, tumors and  
CC AIDS, etc., and tissues or organs that express the protein are useful for  
CC transplantation into humans or other mammals, as allo-, auto- or xeno-  
CC transplants. Also transgenic animals that express the fusion proteins are  
CC useful as source of cells, tissues and organs for transplantation or to  
CC screen for pharmaceuticals and/or to identify toxic substances. The  
CC present sequence is a coding sequence used in the exemplification of the  
CC invention.

SQ Sequence 1108 BP; 342 A; 255 C; 254 G; 257 T; 0 U; 0 Other;

Query Match 47.2%; Score 700.2; DB 12; Length 1108;  
Best Local Similarity 93.2%; Pred. No. 2.6e-178;  
Matches 732; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 700 AAAGAGCTCCAGGCGCTGGAGAGGAAATGCACAGCTGGAATGGAGTTGCAAGCACTG 759  
Db 319 AAAGAGCTGGAGAACTGGAGGAAATATTAAGAAATTTTGGACAGTTTGTATCAT 378  
QY 760 GAAAGAGAACTGGCTCAGGCACAGCATCTGAGCCAGAGGGCCCAATCAAGCCCTGTCT 819  
Db 379 ATTGTCGACATGTTTCATCAACACTTCGGATCCAGAGGGCCCAATCAAGCCCTGTCT 438  
QY 820 CCATGCAAAATGCCAGACACCTTAACCTCTTGGGTGGACCAATCCGCTTTCATCTCCCTCA 879  
Db 439 CCATGCAAAATGCCAGACACCTTAACCTCTTGGGTGGACCAATCCGCTTTCATCTCCCTCA 498  
QY 880 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGTGTGTGAT 939  
Db 499 AAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGTGTGTGAT 558  
QY 940 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTAGCTGGTTTGTGAACAACTGGAAGTACAC 999  
Db 559 GTGAGCGAGGATGACCCAGATGTCCAGATCAGCTAGCTGGTTTGTGAACAACTGGAAGTACAC 618  
QY 1000 ACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCAAGTCC 1059  
Db 619 ACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGGGTGGTCAAGTCC 678  
QY 1060 CTCCCATCCAGCACCAGGACTGGATGAGTGGCAGAGGATTCAATGCAAGGTCAACAA 1119  
Db 679 CTCCCATCCAGCACCAGGACTGGATGAGTGGCAGAGGATTCAATGCAAGGTCAACAA 738  
QY 1120 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 1179  
Db 739 AAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAAGTAAAGCT 798  
QY 1180 CCACAGGTATATGTCTTGCTCCACCGAAGAGAGATGACTAAGAAACAGGTCACTCTG 1239  
Db 799 CCACAGGTATATGTCTTGCTCCACCGAAGAGAGATGACTAAGAAACAGGTCACTCTG 858  
QY 1240 ACCTGCATGGTCACAGACTTCATGCTGCAAGACATTTAGTGGAGTGACCAACACGG 1299  
Db 859 ACCTGCATGGTCACAGACTTCATGCTGCAAGACATTTAGTGGAGTGACCAACACGG 918  
QY 1300 AAAACAGAGCTAAATCTACAAGAACTGAACAGCTCTGGACTCTGATGGTCTTACTTC 1359  
Db 919 AAAACAGAGCTAAATCTACAAGAACTGAACAGCTCTGGACTCTGATGGTCTTACTTC 978  
QY 1360 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCTGT 1419  
Db 979 ATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCTGT 1038  
QY 1420 TCAGTGGTCCAGAGGGTCTGCAGAACTACACACAGACTTAAGAGCTTCTCCGGACTCG 1479  
Db 1039 TCAGTGGTCCAGAGGGTCTGCAGAACTACACACAGACTTAAGAGCTTCTCCGGACTCG 1098  
QY 1480 GGTA 1484  
Db 1099 GGTA 1103



RESULT 10	
ADL15694	
ID	ADL15694 standard; DNA; 990 BP.
XX	
AC	ADL15694;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	Murine immunoglobulin heavy chain constant region DNA SeqID 68.
XX	
KW	mouse; murine; antibody; gene; ds; beta-amyloid; A-beta;
KW	amyloid beta A4 precursor protein; APP; presenilin;
KW	lipoprotein receptor related protein; LRP; beta-amyloid 42; A-beta 42;
KW	Alzheimer's disease; neuroprotective; nootropic.
XX	
OS	Mus musculus.
XX	
PN	W02004018997-A2.
XX	
PD	04-MAR-2004.
XX	
PF	20-AUG-2003; 2003WO-US026173.
XX	
PR	20-AUG-2002; 2002US-0405417P.
PR	18-SEP-2002; 2002US-0411974P.
PT	(NEUR-) NEUROGENETICS INC.
PA	
XX	
PI	Kounnas M, Patrick A, Velicelebi G, Wagner S;
XX	
DR	WPI; 2004-226902/21.
DR	P-PSDE; ADL15695.
XX	
PT	New polypeptide comprises a sequence of amino acids that is selectively
PT	reactive with beta-amyloid peptide 42 or at least one complementarity-
PT	determining region of antibody A387 or B436, useful for treating
PT	Alzheimer's disease.
XX	
PS	Disclosure; SEQ ID NO 68; 408pp; English.
XX	
CC	This invention relates to novel methods and compositions for detecting of
CC	and modulating beta-amyloid (A-beta) peptide levels and the processing of
CC	anyloid beta A4 precursor protein (APP). Specifically, it refers to
CC	methods of assessing the presenilin activity of compounds using the
CC	lipoprotein receptor related protein (LRP) in order to identify
CC	presenilin proteins that can be used to affect the processing of APP. The
CC	present invention describes methods to identify agents that modulate
CC	presenilin activity and A-beta levels, in particular beta-amyloid 42 (A-
CC	beta 42), such that the agent is selectively reactive with A-beta 42 and
CC	binds at least one complementarity determining region (CDR) of either
CC	antibody A387 or antibody B436. As such, the polypeptides, nucleic acids
CC	and antibodies are useful for treating Alzheimer's disease, accordingly
CC	the compositions exhibit neuroprotective and nootropic activities. This
CC	polynucleotide sequence is a murine antibody chain DNA fragment of the
CC	invention.
XX	
SQ	Sequence 990 BP; 274 A; 286 C; 235 G; 195 T; 0 U; 0 Other;
	Query Match 47.1%; Score 699.6; DB 12; Length 990;
	Best Local Similarity 100.0%; Pred. No. 3.6e-178;
	Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	786 TGAGCCAGAGGGCCCAATCAAGCCCTGCTCTCCATGCAAAATGCCAGCACCTAACCT 845
Db	291 TGAGCCAGAGGGCCCAATCAAGCCCTGCTCTCCATGCAAAATGCCAGCACCTAACCT 350
QY	846 CTTGGGTGGACATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 905
Db	351 CTTGGGTGGACATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTC 410
QY	906 CTTGAGCCCATAGTCAATGTGTGGTGGATGTGAGCGAGGATGACCCAGATGTGCA 965





Db 661 CACATACACACACGACTAAGAGCTTCTCCGAGCTCCGGGTAA 704

RESULT 14

AD85817  
ID ADE85817 standard; cDNA; 1140 BP.

AC ADE85817;

DT 29-JAN-2004 (first entry)

DE Murine interleukin-21/Fc fusion gene.

XX Mouse; interleukin-21; immunosuppressive; antirheumatic; antiarthritic;  
XX antiinflammatory; dermatological; ophthalmological; uropathic;  
KW muscular-gen.; vasotropic; antidiabetic; antithyroid; thyromimetic;  
KW neuroprotective; gastrointestinal-gen.; antipsoriatic; gene therapy;  
XX antibody; antibody; gene; ss.

XX Chimeric.

OS Mus sp.

XX Key Location/Qualifiers  
FH 1. 1140  
FT CDS  
FT /\*tag= a  
FT /product= "IL-21/Fc fusion"

XX WO2003087320-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-US010736.

XX 09-APR-2002; 2002US-0371038P.

XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Moll T, Strom TB, Zheng XX;

XX WPI; 2003-845317/78.

XX P-PSDB; ADE85818.

XX New substantially pure interleukin-21 polypeptide, useful for diagnosing,  
XX treating and prognosticating autoimmune disorders, e.g. rheumatic  
XX disease, type I diabetes, Graves disease, multiple sclerosis, psoriasis  
XX and myasthenia gravis.

XX Disclosure; SEQ ID NO 10; 65pp; English.

XX The present sequence is the coding sequence for a fusion protein  
XX comprising murine interleukin-21 (IL-21) and an immunoglobulin Fc  
XX polypeptide. Murine IL-21/Fc is capable of transducing signals through  
XX the murine IL-21 receptor, has an increased in vivo serum half-life and  
XX can activate complement mediated lysis or antibody-dependent cellular  
XX cytotoxicity. The invention provides antagonists of the IL-21 receptor.  
XX These include mutants of murine IL-21 and additionally comprise a  
XX sequence that increases circulating half-life, such as the Fc region of  
XX an IgG molecule. Such antagonists inhibit cellular proliferation in  
XX response to either anti-CD3 monoclonal antibodies or anti-CD3 antibodies  
XX applied together with IL-2 and/or IL-15 together with IL-21. A claimed  
XX method of suppressing the immune response in a patient comprises  
XX administering the IL-21 antagonist or a nucleic acid encoding it. The  
XX method is used to treat an autoimmune disease such as rheumatic disease,  
XX including systemic lupus erythematosus, Sjogren's syndrome, scleroderma,  
XX mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's  
XX syndrome, or Behcet's disease, or rheumatoid arthritis, type I diabetes,  
XX autoimmune disease of the thyroid such as Hashimoto's thyroiditis or  
XX Graves' disease, an autoimmune disease of the central nervous system such  
XX as multiple sclerosis, myasthenia gravis, or encephalomyelitis, or an  
XX autoimmune disease selected from pemphigus vulgaris, pemphigus vegetans,  
XX pemphigus foliaceus, Senechal-Usher syndrome, Brazilian pemphigus,  
XX psoriasis or inflammatory bowel disease (all claimed).

XX SQ Sequence 1140 BP; 344 A; 296 C; 264 G; 236 T; 0 U; 0 Other;  
Query Match 47.1%; Score 699.2; DB 10; Length 1140;  
Best Local Similarity 97.5%; Pred. No. 4.9e-178;  
Matches 710; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 757 CTGGAAAGGAAGTGGCTCAGGCAGCATCTCAGCCAGAGGGCCACAAATCAAGCCCTGT 816  
DB 409 CTTCAAAAGATGATTCATCAGCATCTCTCAGATCCAGAGGGCCACAAATCAAGCCCTGT 468  
QY 817 CCTCATCAAAATGCCAGACCACTTCTTGGTGAGACCATCCGTCTTCATCTTCCCT 876  
DB 469 CTTCAATCAAAATGCCAGACCACTTCTTGGTGAGACCATCCGTCTTCATCTTCCCT 528  
QY 877 CCAAAGATCAAGGATGATCATGATCTCCCTGAGCCCCCAGTAGTCACATGTGTGTGGTG 936  
DB 529 CCAAAGATCAAGGATGATCATGATCTCCCTGAGCCCCCAGTAGTCACATGTGTGTGGTG 588  
QY 937 GATGTGAGGAGGATGACCCAGATGTCAGATCAGCTGTTTGTGAAACAACGTGGAAGTA 996  
DB 589 GATGTGAGGAGGATGACCCAGATGTCAGATCAGCTGTTTGTGAAACAACGTGGAAGTA 648  
QY 997 CACACAGCTCAGACACAAACCCATAGAGAGGATTACAAACAGTACTCTCCGGGTGTCTAGT 1056  
DB 649 CACACAGCTCAGACACAAACCCATAGAGAGGATTACAAACAGTACTCTCCGGGTGTCTAGT 708  
QY 1057 GCGCTCCCATCCAGCAGGAGTGGATGATGGCAAGGAGTTCAAAATGCAAGGTCAAC 1116  
DB 709 GCGCTCCCATCCAGCAGGAGTGGATGATGGCAAGGAGTTCAAAATGCAAGGTCAAC 768  
QY 1117 AACAAAGACCTCCAGAGCCCATCGAGAGACCATCTCAAAACCCAAAGGGTCACTAAGA 1176  
DB 769 AACAAAGACCTCCAGAGCCCATCGAGAGACCATCTCAAAACCCAAAGGGTCACTAAGA 828  
QY 1177 GCTCCACAGGTATATGTCTTGCCTCCACAGAGAGAGATGACTTAAGAAACAGGTCACT 1236  
DB 829 GCTCCACAGGTATATGTCTTGCCTCCACAGAGAGAGATGACTTAAGAAACAGGTCACT 888  
QY 1237 CTGACCTGTCATGGTCAACAGACTTTCATGCTGAAAGACATTTAGTGGAGTGGAACCAAC 1296  
DB 889 CTGACCTGTCATGGTCAACAGACTTTCATGCTGAAAGACATTTAGTGGAGTGGAACCAAC 948  
QY 1297 GGGAAACAGAGCTAAACTACAAGACACTGAACCGAGTCTCTGGACTCTGTAGTGTCTTAC 1356  
DB 949 GGGAAACAGAGCTAAACTACAAGACACTGAACCGAGTCTCTGGACTCTGTAGTGTCTTAC 1008  
QY 1357 TTCAATGTACAGAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTTCC 1416  
DB 1009 TTCAATGTACAGAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTTCC 1068  
QY 1417 TGTTCAAGTGGTCCAGAGGGTCTGCACAATCAACACAGACTTAAGAGACTTCTCCCGGACT 1476  
DB 1069 TGTTCAAGTGGTCCAGAGGGTCTGCACAATCAACACAGACTTAAGAGACTTCTCCCGGACT 1128  
QY 1477 CCGGGTAA 1484  
DB 1129 CCGGGTAA 1136  
RESULT 15  
ID AAT59350 standard; DNA; 1158 BP.  
XX AC AAT59350;  
XX DT 07-MAY-1997 (first entry)  
XX DE 1-153 delta 112-115 c-mpl ligand-mouse Fc fusion gene.  
XX KW c-mpl ligand; Megakaryocyte Growth and Development Factor; MGDF;  
XX thrombopoietin; TPO; variant; mutein; chimera; increased activity;  
XX decreased side effect; ex vivo expansion; stem cell; treatment;

haematopoietic disorder; gene therapy; human; ss.

KW XX

OS Synthetic.

OS Mus sp.

OS Chimeric.

XX

PN WO9623888-A1.

XX

XX 08-AUG-1996.

XX

PF 01-FEB-1996; 96WO-US000830.

XX

PR 03-FEB-1995; 95US-00383035.

XX

PA (SEAR ) SEARLE & CO G D.

XX

PI Staten NR, Favara JP, Kahn LE, Baum CM, Pegg LE, McKearn JP;

XX

DR WPI; 1996-371436/37.

DR P-PSDB; AAW01765.

XX

PT Mutant c-mpl ligands - used for stimulating the prodn. of haematopoietic

PT cells and in the treatment of haematopoietic disorders.

XX

PS Claim 20; Page; 74pp; English.

XX

CC This DNA sequence, isolated from BHK expression plasmid pMON26465,  
CC encodes amino acids 1-153 of c-mpl ligand with a deletion of residues 112  
CC -115 fused to a mouse Fc fragment. The native c-mpl ligand is also  
CC referred to as Megakaryocyte Growth and Development Factor (MGDF) or  
CC thrombopoietin (TPO). Variants and chimera of c-mpl ligand can have an  
CC improved biological profile, such as increased activity and/or decreased  
CC side effects, and/or improved physical properties, such as improved half-  
CC life, stability and/or re-fold efficiencies. They can be used for  
CC selective ex vivo expansion of stem cells, for the treatment of patients  
CC having a haematopoietic disorder or in human gene therapy

XX

SQ Sequence 1158 BP; 299 A; 333 C; 291 G; 235 T; 0 U; 0 Other;

Query Match 47.1%; Score 699; DB 2; Length 1158;

Best Local Similarity 100.0%; Pred. No. 5.6e-178;

Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

786 TGAGCCAGAGGGCCACAAATCAAGCCCTGTCCTCCATGCAAAATGCCAGCACCTAACCT 845

Db

459 TGAGCCAGAGGGCCACAAATCAAGCCCTGTCCTCCATGCAAAATGCCAGCACCTAACCT 518

Qy

846 CTTGGGTGGACCAATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGATCATGATCTC 905

Db

519 CTTGGGTGGACCAATCCGCTCTTCATCTTCCCTCCAAAGATCAAGGATGATCATGATCTC 578

Qy

906 CTTGAGCCCNATGATCATGTTGGTGGTGGATGTGAGGAGGATGACCCAGATGCCA 965

Db

579 CTTGAGCCCNATGATCATGTTGGTGGTGGATGTGAGGAGGATGACCCAGATGCCA 638

Qy

966 GATCAGCTGTTTGTGAACACGTTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 1025

Db

639 GATCAGCTGTTTGTGAACACGTTGGAAGTACACACAGCTCAGACACAAACCCATAGAGA 698

Qy

1026 GGATTACACAGTACTCTCCGGGTGGTCAAGTGCCTCCATCCAGCACCCAGGACTGGAT 1085

Db

699 GGATTACACAGTACTCTCCGGGTGGTCAAGTGCCTCCATCCAGCACCCAGGACTGGAT 758

Qy

1086 GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGGCCCATCGAGAG 1145

Db

759 GAGTGGCAAGAGTTCAAAATGCAAGGTCAACAAAGAGCTCCAGGCCCATCGAGAG 818

Qy

1146 AACCATCTCAAAACCCAAAGGTCAGTAAGAGCTCCAGGTATATCTTGCCTCCACC 1205

Db

819 AACCATCTCAAAACCCAAAGGTCAGTAAGAGCTCCAGGTATATCTTGCCTCCACC 878

Qy

1206 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGATGGTCAAGACTTCATGCC 1265

Db 879 AGAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGATGTCAAGACTTCATGCC 938

Qy 1266 TGAAGACATTTTACCTGGAGTGGACCAACAAACGGGAAAAACAGAGCTAAACTACAAGAACAC 1325

Db 939 TGAAGACATTTTACCTGGAGTGGACCAACAAACGGGAAAAACAGAGCTAAACTACAAGAACAC 998

Qy 1326 TGAACCAAGTCTCTGAGCTCTCATGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1385

Db 999 TGAACCAAGTCTCTGAGCTCTCATGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAA 1058

Qy 1386 GAAGAACTGGGTGGAAAGAAATAGCTACTCTGTTTCAGTGGTCCACGAGGGTCTGCACAA 1445

Db 1059 GAAGAACTGGGTGGAAAGAAATAGCTACTCTGTTTCAGTGGTCCACGAGGGTCTGCACAA 1118

Qy 1446 TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA 1484

Db 1119 TCACCACACGACTAAGAGCTTCTCCCGGACTCCCGGGTAA 1157

Search completed: June 19, 2005, 11:25:31

Job time : 889 secs

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Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	2655	98.5	494	4	AA967480	Aab67480 A fusion
2	2242	83.2	551	4	AB956471	AB956471 Murine pC
3	1919.5	71.2	479	2	AA931654	AA931654 HLA-DR2 a
4	1733	64.3	774	4	AB956461	AB956461 IAS MBP 1
5	1732.5	64.3	772	4	AB956463	AB956463 IAS MBP 9
6	1521	56.4	676	4	AB956458	AB956458 IAS MBP 1
7	1521	56.4	678	4	AB956457	AB956457 IAS MBP 1
8	1327	49.2	426	8	ADJ15170	ADJ15170 Murine mo
9	1319.5	49.0	469	2	AAR40384	AAR40384 Monoclonal
10	1313.5	48.7	468	2	AAR13061	AAR13061 Monoclonal

XX PS XX Example 1; Page 31-33; 43pp; French.

XX The specification describes soluble recombinant proteins that comprise at least a dimer formed from the alpha and beta-chains of MHC (major histocompatibility complex) Class I and II molecules in which at least one chain has, attached to its C-terminus, at least part of the FC region of an immunoglobulin. The recombinant proteins, when linked to an antigenic peptide, are used to count and/or purify antigen-reactive T lymphocytes and to characterize their phenotype, e.g. in preclinical evaluation of vaccines. They are also used as immunostimulants, particularly for vaccine development (against infections and tumours), to count and determine phenotype of autoreactive T cells in subjects with, or at risk of developing, autoimmune diseases, e.g. for staging or evaluating treatments, and (to purify and/or enrich Ag-reactive T cells from cell cultures or patient samples, for use in subsequent curative or preventative cellular therapy. The present sequence represents a recombinant protein of the invention, comprising an alpha chain of MHC molecules

XX SQ Sequence 494 AA;

Alignment Scores:

Pred. No.:	3.48e-215	Length:	494
Score:	2655.00	Matches:	494
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	98.52%	Indels:	0
DB:	4	Gaps:	0

US-10-048-116-1 (1-1484) x AAB67480 (1-494)

Qy	1	ATGCGGTGACAGAGCTCTGATCTGGGGTCTCCGCCCTGAACACCATGCTCAGCCTC	60
Db	1	MetProCysSerArgAlaLeuIleLeuGlyValLeuAlaLeuAenThrMetLeuSerLeu	20
Qy	61	TGCGGAGGTGAAGACGACATTGAGCCGACACCTAGGCTCTATGGTACAACTGTTTAT	120
Db	21	CysGlyGlyGluAspAspIleGluAlaAspHisValGlyPheTyrGlyThrValTyr	40
Qy	121	CAGTCTCTCGAGACATTGGCCAGTACACATCAATTTGATGGTGTAGTCTGTTCTAT	180
Db	41	GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr	60
Qy	181	GTGACTTGGATAGAGAAACCTGTCTGGAGGCTTCTGAGTTTGGCCAAATGATCTC	240
Db	61	ValAspLeuAspLysLysThrValTyrArgLeuProGluPheGlyGlnLeuIleLeu	80
Qy	241	TTTGAGCCCCAAGTGGACTGCNAACATAGCTCCAGAAACACAACTTGGGAATCTTG	300
Db	81	PheGluProGlnGlyLeuGlnAsnIleAlaAlaGluLysHisAsnLeuGlyIleLeu	100
Qy	301	ACTAAGAGGTCAAATTTCAACCCAGCTACCAATAGGCTCTCAAGGACTGTGTTCCCC	360
Db	101	ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro	120
Qy	361	AAGTCCCTGTGCTGCTGGTGACCCCAACCCCTTATCTGCTTTGTGGCAACATCTTC	420
Db	121	LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe	140
Qy	421	CCACCTGTGATCAACATCAGCTGCTCAGAAATAGCAAGTCAGTCACAGCGGGTTAT	480
Db	141	ProProValIleAenIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr	160
Qy	481	GAGACCACTCTCTCGTCAACCGTGACCATTCCTTCCACAAAGCTGTCTTCTCACCTTC	540
Db	161	GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe	180
Qy	541	ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGACCG	600
Db	181	IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro	200
Qy	601	GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCTGAGACTGACAGAACTGGA	660

Db	201	ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThrGly	220
Qy	661	GGTGGAGGATCCACTACAGCTCCATCAGCTCGAGCTCGAAAAAGAGCTCCAGCGCCTGGAG	720
Db	221	GlyGlyGlySerThrThrAlaProSerAlaGlnLeuGluLysGluLeuAlaLeuGlu	240
Qy	721	AAGGAAAATGCACAGCTGGAAATGGAGTTGCAAGCATCTGAAAGAAAGAACTGGCTCAGGCA	780
Db	241	LysGluAsnAlaGlnLeuGluTrpGluLeuAlaLeuGluLysGluLeuAlaGlnAla	260
Qy	781	GCATCTCAGCCAGAGGGCCCAATCAAGCCCTGCTCCATGCAATGCAATGCCAGCACCT	840
Db	261	AlaSerGluProArgGlyProThrIleLysProCysProProCysLysCysProAlaPro	280
Qy	841	AACCTCTTGGGTGACCATCCGCTTCTCATCTTCCTCCAAAGATCAAGAGTGTACTCATG	900
Db	281	AsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeuMet	300
Qy	901	ATCTCCCTGAGCCCATAGTCAATGTCATGTGTGGTGTGATGTGAGCGAGGATGACCCAGAT	960
Db	301	IleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspProAsp	320
Qy	961	GTCCAGATCAGCTGGTTGTGAACACGTCGAAAGTACACACAGCTCAGACACAAACCAT	1020
Db	321	ValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnHis	340
Qy	1021	AGAGAGGATTACAAACAGTACTCTCCGGGTGGTCTAGTGTCCCTCCCATCCAGCACAGGAC	1080
Db	341	ArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAsp	360
Qy	1081	TGATGATGGCAAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCAGCGCCCATC	1140
Db	361	TrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaProIle	380
Qy	1141	GAGAGACCATCTCAAAACCCAAAGGTCAGTAAGACTCCACAGGTATATGCTTCGCT	1200
Db	381	GluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeuPro	400
Qy	1201	CCACCAAGAAGAGATGACTAAGAAACAGGTCACTCTGACCTGCTGCTGCTGCTGCTGCT	1260
Db	401	ProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAspPhe	420
Qy	1261	ATGCTGCAAGACATTTACGTGGAGTGACCAACACCGGAAACACAGACTAAACTACAAG	1320
Db	421	MetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLys	440
Qy	1321	AACACTGAACCCAGTCTGAGCTCTGATGTTTCTTACTTCTATGTCACAGCAAGCTCAGAGTG	1380
Db	441	AsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgVal	460
Qy	1381	GAAGAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTTTCTGAGTGGTCCAGGGGCTG	1440
Db	461	GluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeu	480
Qy	1441	CACAATCACCACAGCACTAAGAGCTTCTCCGGACTCCGGGT	1482
Db	481	HisAsnHisHisThrThrLysSerPheSerArgThrProGly	494

RESULT 2

ABB56471

ID ABB56471 standard; protein; 551 AA.

XX ABB56471;

XX 25-FEB-2002 (first entry)

XX Murine pCB223 protein.

XX Mouse; MHC; major histocompatibility complex; MHC class II; multimer;  
 KW single chain; immunosuppressive; antidiabetic; antiinflammatory;  
 KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;  
 KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;

KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;  
 XW rheumatoid arthritis; systemic lupus erythematosus.

OS Mus sp.  
 OS Synthetic.

XX WO200170245-A1.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US009616.

XX 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.

PR 23-JAN-2001; 2001US-0264003P.

XX (CORI-) CORIXA CORP.

XX Carter D, Zhu S, Arimilli S, Wang A;

XX WPI; 2001-616371/71.

DR N-PSDB; ABI99041.

XX Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha1 and beta1 domain linked through amino acid linker and multimerization domain.

PT Disclosure; Page 124-125; 147pp; English.

XX The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha1 domain and a beta1 domain linked through an amino acid linker and a multimerization domain. The first and the second molecule are linked through the multimerization domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence is a single chain MHC class II molecule of the invention

XX Sequence 551 AA;

SQ Alignment Scores:

Pred. No.:	2-78e-180	Length:	551
Score:	2242.00	Matches:	431
Percent Similarity:	81.17%	Conservative:	13
Best Local Similarity:	78.79%	Mismatches:	39
Query Match:	83.19%	Indels:	64
DB:	4	Gaps:	5

US-10-048-116-1 (1-1484) x ABB56471 (1-551)

QY	19	CTGATTCGGGGTCTCGCCCTGAAACACCATGCTCAGCTCTGCGGA-----GGTGAA	72
DB	9	LeuLeuSerAlaAlaValValLeuMetValLeuSerSerProGlyThrGluGlyGlu	28
QY	73	GAGCAGATTGAGCCGACCACTAGGCTTCTATGGTACAACTGTTATCATGCTCTCTGGA	132
DB	29	AspAspIleGluAlaAspHisValGlyValTyrGlyThrValTyrGlnSerProGly	48
QY	133	GACATTGGCCAGTACACATGAATTTGATGGTGATGAGTTGTTCTATGTGGACTTGGAT	192
DB	49	AspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrpPheThrValAspLeuAsp	68
QY	193	AAGAAGAAACTCTCTGGAGGCTTCCTAGTCTTGGCCAAATTGATCTTTTGAGCCCCAA	252
DB	69	LysLysGluThrIleTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspProGln	88
QY	253	GGTGGACTGCAAAACATAGCTGCAGAAAACACAACTTGGGAATCTTGACTAAGAGGTCA	312
DB	89	GlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGlyIleLeuThrLysArgSer	108

QY	313	AATTTCACCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCTCCCAAGTCCCTGTG	372
DB	109	AsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerProVal	128
QY	373	CTGCTGGGTGAGCCCAACACCCCTTATCTGCTTTGTGGACAACATCTTCCACCTGTGATC	432
DB	129	LeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProValIle	148
QY	433	AACATCACATGGCTCAGAAATAGCAAGTCAGTCACAGAGCGCGTTTATAGACAGCTTC	492
DB	149	AsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSerPhe	168
QY	493	CTGCTCAACCGTGACCATTCCTTCCACAAGCTGCTTATCTCACTTCATCTTCTGAT	552
DB	169	LeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSerAsp	188
QY	553	GATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTTGAGAGCGCGTTCTGAAACAC	612
DB	189	AspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluProValLeuLysHis	208
QY	613	TGGGACCTGAGATTCACGCCCATGTGAGAGCTGACAGAACTGGAGGTGGAGGATCC	672
DB	209	TrpGluProGluIleProAlaProMetSerGlu-----GlySerAlaLys	223
QY	673	ACTACAGCTCCATCA-----	687
DB	224	ThrAlaProSerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSer	243
QY	687	-----	687
DB	244	ValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThrLeuThrTrpAsn	263
QY	688	-----GCTCAGCTCGAAAGAGCTCCAG	711
DB	264	SerGlySerLeuSerSerGlyValHisThrPheProAlaValLeuGlnSerAspLeuTyr	283
QY	712	GCCTCGAGAGGAA-----AATGCACAGCTGGAATGGAGTGGCAAGACACTCGAAAAG	765
DB	284	ThrLeuSerSerSerValThrValThrSerSerThrTrpProSerGlnSerIleThrCys	303
QY	766	GAACTGGCTCAGCAGCATCT-----GAGCCCAAGGAGGCC	801
DB	304	AsnValAlaHisProAlaSerThrLysValAspLysLysIleGluProArgGlyPro	323
QY	802	ACAATCAAGCCCTGCTCCTCATGCAATGCCAGCACCTAACCTCTGGGTGACCATCC	861
DB	324	ThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGlyGlyProSer	343
QY	862	GTCTTCATCTTCCCTCCAAAGATCAAGGATGTACTCATGATCTCCTGAGCCCCATAGTC	921
DB	344	ValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerProIleVal	363
QY	922	ACATGTGTGGTGTGATGTGAGCGAGGATGACCCAGATGTCCAGATGAGCTGGTTGTG	981
DB	364	ThrCysValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheVal	383
QY	982	AACAAGTGGAGTACACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACT	1041
DB	384	AsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThr	403
QY	1042	CTCCGGGTGGTGTGATGCTCCCTCCCATCCAGCACAGGACTGGATGAGTGGCAAGGATTC	1101
DB	404	LeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPhe	423
QY	1102	AAATGCAAGGTCAACAACAAGACCTCCAGCGCCCATCCAGAGAACCATCTCAAAACCC	1161
DB	424	LysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLysPro	443
QY	1162	AAAGGTGAGTAAAGAGCTCCACAGGTATATGCTTCCTCCACCAAGAGAGAGTACT	1221
DB	444	LysGlySerValArgAlaProGlnValTyrValLeuProProProGluGluMetThr	463



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Db 164 AspValTyrAspCysArgValGluHisTrpGlyLeuAspGluProLeuLeuLeuHisTrp 183
QY 616 GAACCTTGAGATTCCAGCCCGCCATGTCAGAGCTCAGCAAACT--CGAGGTGAGGATCC 672
Db 184 GluPheAspAlaProSerProLeuProGluThrThrGluValAspGlyGlyGlyGly 203
QY 673 ACTACA-----GCTCCATCAGCTCAGCTCGAAAGAGAGCTCCAGGCGCCCTGGAG 720
Db 204 LeuThrAspThrLeuGlnAlaGluThrAspGlnLeuGluAspGluLysSerAlaLeuGln 223
QY 721 AAGGAAATCCACAGCTGGGAATGGGAGTTCCAGACGCTGGAAGAACTG---GCTCAG 777
Db 224 ThrGluIleAlaAsnLeuLeuLysGluLysGluLysLeuGluPheIleLeuAlaHis 243
QY 778 GCAGCATCTGAGCCCGAGGCGCCAACTCAAGCCCTGCTCCATCGCAAAATGCCAGCA 837
Db 244 AlaAlaSerGluProArgGlyProThrIleLysProCysProCysLysCysProAla 263
QY 838 CCTAACCTCTTGGGTGGACCATCCGCTTTCATCTTCCCTCCAAAGATCAAGGATGTACTC 897
Db 264 ProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAspValLeu 283
QY 898 ATGATCTCCCTGAGCCCGCCATGATGATGATGATGATGATGATGATGATGATGATGATG 957
Db 284 MetIleSerLeuSerProIleValThrCysValValValAspValSerGluAspAspPro 303
QY 958 GATGTCAGATCAGCTGTTGTTGGAACAGCTGGAAGTACACACAGCTCAGACACAAACC 1017
Db 304 AspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThr 323
QY 1018 CATAGAGAGGATTACACAGTACTCTCCGGGTGGTCTAGTCCCTCCCTCCAGCACCAAG 1077
Db 324 HisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGlnHisGln 343
QY 1078 GACTGATGATGGGAGGAGTTCAATGCAAGGTCAACAAAGACCTCCAGCGGCC 1137
Db 344 AspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuProAlaPro 363
QY 1138 ATCGAGAGAACCTCTCAAAACCAAGGTCAGTAAAGCTCCAGGCTCCAGGTTATGCTTG 1197
Db 364 IleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyrValLeu 383
QY 1198 CTCCACCAAGAGAGATGACTAAAGAAACAGGTCACTCTGACCTGCATGGTCACAGAC 1257
Db 384 ProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetValThrAsp 403
QY 1258 TTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAACGGGAAACAGAGCTAAACTAC 1317
Db 404 PheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyr 423
QY 1318 AAGAACACTGAACCTGCTGAGCTCTGATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1377
Db 424 LysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArg 443
QY 1378 GTGGAAGAAAGAACTGGGTGGGAAAGAAATAGTACTCTCTGTTTCAGTGGTCCACAGGGT 1437
Db 444 ValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGly 463
QY 1438 CTGCACAATCACCACAGCTAAGAGCTTCTCCCGAGCTCCGGT 1482
Db 464 LeuHisAsnHisThrThrLysSerPheSerArgThrProGly 478

```

## RESULT 4

ABB56461

ID ABB56461 standard; protein; 774 AA.

XX AC ABB56461;

XX DT 25-FEB-2002 (first entry)

XX DE IAS MBP 1-14 CK protein.

XX

Mus; MHC; major histocompatibility complex; MHC class II; multimer; single chain; immunosuppressive; antidiabetic; neuroinflammatory; antianemic; antirheumatoid; antiarthritic; neuroprotective; vaccine; autoimmune disease; insulin dependent diabetes; multiple sclerosis; myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis; rheumatoid arthritis; systemic lupus erythematosus.

Mus sp.

Synthetic.

WO200170245-A1.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US009616.

XX 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.

PR 23-JAN-2001; 2001US-0264003P.

XX (CORI-) CORIXA CORP.

XX Carter D, Zhu S, Arimilli S, Wang A;

PI WPI; 2001-616371/71.

XX N-PSDB; ABI99031.

DR Multimeric complex for treating autoimmune diseases, comprises first and second single chain MHC class II molecules, each comprising alpha and beta domain linked through amino acid linker and multimerization domain.

XX Example 7; Page 105-107; 147pp; English.

PS The invention relates to a multimeric complex comprising a first recombinant single chain major histocompatibility complex (MHC) class II molecule and a second recombinant single chain MHC class II molecule, each comprising an alpha domain and a beta domain linked through an amino acid linker and a multimerization domain. The first and the second molecule are linked through the multimerization domain to form a multimeric complex. The complex is useful for treating autoimmune diseases. It is useful for treating insulin dependent diabetes, multiple sclerosis, myasthenia gravis, pernicious anaemia, autoimmune encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus erythematosus. The present sequence is a single chain MHC class II molecule of the invention

XX Sequence 774 AA;

SQ

Alignment Scores:

Pred. No.: 3.08e-137 Length: 774

Score: 1733.00 Matches: 335

Percent Similarity: 70.71% Conservative: 44

Best Local Similarity: 62.50% Mismatches: 79

Query Match: 64.30% Indels: 78

DB: 4 Gaps: 8

US-10-048-116-1 (1-1484) x ABB56461 (1-774)

QY 64 GSAGGT-----GAAGACACATTGAGCGCGACCATGCTTCTTGTGACACT 114

Db 253 GlyGlySerSerSerGluAspAspIleGluAlaAspHisValGlyValTyrGlyThrThr 272

QY 115 GTTTATCAGTCTCTCGAGACATTGGCCAGTACACACATGAATTTGATGTTGATGTTG 174

Db 273 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrp 292

QY 175 TTCTATGTGGACTTGGATAAGAGAAACTGTCTGGAGGCTTCTCTGAGTTTGGCCAAATG 234

Db 293 PheTyrValAspLeuAspLysLysGluThrIleTrpMetLeuProGluPheGlyGlnLeu 312

QY 235 ATACTCTTTGAGCCCCCAAGGTGACATGCGAAAACATAGCTGCGAAAACACAACTTGGGA 294

Db 313 ThrSerPheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly 332

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QY 295 ATCTTGACTAAGAGGTCAAAATTTACCCAGCTACCAATGAGGCTCTCTCAAGCAGCTGTG 354
Db 333 IleLeuThrLysArgSerThrProAlaThrAsnGluAlaProGlnAlaThrVal 352
QY 355 TTCCCAAGTCCCTGCTGCTGGTCCAGCCCAACACCCCTTATCTGCTTTGTGGACAAC 414
Db 353 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 372
QY 415 ATCTTCCACCTGTGATCAACATCACATGGCTGCAGAAATAGCAAGTCAGTCACAGACGC 474
Db 373 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValIleAspGly 392
QY 475 GTTTATGAGACAGCTTCTCTGTCACCCGTGACCATTCCTTCCACAGACTGCTTATCTC 534
Db 393 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 412
QY 535 ACCTTCATCCCTCTGATGATGACATTTATCACTGCAAGGTGGACACTGGGGCTGGAG 594
Db 413 ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 432
QY 595 GAGCCGGTTCTGAACACTGGGAACCTGAGATTCCAGGCCCTCATGTCCAGAGCTGACAGAA 654
Db 433 GluProValLeuLysHisTrp-----Ala 440
QY 655 ACTGGAGTGGAGATCC-----ACTACAGCTCCATCA----- 687
Db 441 SerGlyGlyGlyGlySerGlyGlyGlyAlaLysThrThrProProSerValTyrPro 460
QY 687 ----- 687
Db 461 LeuAlaProGlySerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuValLys 480
QY 687 ----- 687
Db 481 GlyTyrPheProGluProValThrValThrTrpAsnSerGlySerLeuSerSerGlyVal 500
QY 688 -----GCTCAGCTGAAAAGAGACTCCAGGCCCTGGAGAGGAAAATGCA--- 732
Db 501 HisThrPheProAlaValLeuGlnSerAspLeuThrLeuSerSerValThrVal 520
QY 733 ---CAGCTGGAATGGAGTTCCAGCAGCTGAAAAGAACTGGCTCAGGACGATCTGAG 789
Db 521 ProSerSerThrTrpProSerGluThrValThrCysAsnValAlaHisProAlaSerSer 540
QY 790 CCCAGA---GGGCCCAATCAAGCCC-----TCTCCTCCATGCAAAATGCCCA 834
Db 541 ThrLysValAspLysLysIleValProArgAspCysGlyCysLysProCysIleCysThr 560
QY 835 GCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTCCCTCCAAAGATCAAGATGTA 894
Db 561 ValProGluVal-----SerSerValPheIlePheProProLysPheLysAspVal 577
QY 895 CTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGATGTGAGCAGGATGAC 954
Db 578 LeuThrIleThrLeuThrProLysValThrCysValValValAspIleSerLysAspAsp 597
QY 955 CCAGATGTCAGATCAGCTGTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAA 1014
Db 598 ProGluValGlnPheSerTrpPheValAspAspValGluValHisThrAlaGlnThrGln 617
QY 1015 ACCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTTCAGTGCCTCCCATCAGCAC 1074
Db 618 ProArgGluGluGlnPheAsnSerThrPheArgSerValSerGluLeuProIleMetHis 637
QY 1075 CAGGACTGGATGAGTGGCAAGGATTCAAATGCAAGGTCAACAAAGACCTCCACGCG 1134
Db 638 GlnAspTrpLeuAsnGlyLysGluPheLysCysArgValAsnSerAlaAlaPheProAla 657
QY 1135 CCCATCGAGAGAACCATCTCAAAACCCCAAGGGTCAGTAGAGCTCCACAGGTATATGC 1194
Db 658 ProIleGluLysThrIleSerLysThrLysGlyArgProLysAlaProGlnValTyrThr 677
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QY 1195 TTGCCTCCACGAGAGAGATGACTAAGAAACAGGCTCACTCTGACTCGATCGTCACA 1254
Db 678 IleProProLysGluGlnMetAlaLysAspLysValSerLeuThrCysMetIleThr 697
QY 1255 GACTTTCATGCTGAAGACATTTACGTGGAGTGGACCAACACGGGAAAAACAGAGCTAAAC 1314
Db 698 AspPhePheProGluAspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGluAsn 717
QY 1315 TACAAGAACACTGAACAGCTCGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTG 1374
Db 718 TyrLysAsnThrGlnProIleMetAspThrAspGlySerTyrPheValTyrSerLysLeu 737
QY 1375 AGACTGAAAAGAGAACTGGTGGAAAGAAATAGTACTCTCTCAGTGGTCCAGCAG 1434
Db 738 AsnValGlnLysSerAsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHisGlu 757
QY 1435 GGTCTGCACATCAACACAGCACTAAGAGCTTCTCCCGGACTCCGGGT 1482
Db 758 GlyLeuHisAsnHisThrGluLysSerLeuSerHisSerProGly 773

RESULT 5
ABB56463
ID ABB56463 standard; protein; 772 AA.
AC ABB56463;
XX
XX 25-FEB-2002 (first entry)
XX
XX IAS MBP 90-101 CH1.H.CH2.CH3 protein.
XX
XX Mouse; MHC; major histocompatibility complex; MHC class II; multimer;
XX single chain; immunosuppressive; antidiabetic; antiinflammatory;
XX antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;
XX autoimmune disease; insulin dependent diabetes; multiple sclerosis;
XX myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;
XX rheumatoid arthritis; systemic lupus erythematosus.
XX
XX Mus sp.
XX Synthetic.
XX WO200170245-A1.
XX
XX 27-SEP-2001.
XX
XX 22-MAR-2001; 2001WO-US009616.
XX
XX 22-MAR-2000; 2000US-0191274P.
XX
XX 15-MAY-2000; 2000US-0204249P.
XX
XX 23-JAN-2001; 2001US-0264003P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Carter D, Zhu S, Arimilli S, Wang A;
XX WPI: 2001-616371/71.
XX
XX N-PSDB; ABI99033.
XX
XX Multimeric complex for treating autoimmune diseases, comprises first and
XX second single chain MHC class II molecules, each comprising alpha and
XX beta domain linked through amino acid linker and multimerization domain.
XX
XX Example 7; Page 109-112; 147pp; English.
XX
XX The invention relates to a multimeric complex comprising a first
XX recombinant single chain major histocompatibility complex (MHC) class II
XX molecule and a second recombinant single chain MHC class II molecule,
XX each comprising an alpha domain and a beta domain linked through an
XX amino acid linker and a multimerisation domain. The first and the second
XX molecule are linked through the multimerisation domain to form a
XX multimeric complex. The complex is useful for treating autoimmune
XX diseases. It is useful for treating insulin dependent diabetes, multiple
XX sclerosis, myasthenia gravis, pernicious anaemia, autoimmune
XX encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus
```



CC erythematous. The present sequence is a single chain MHC class II  
 XX molecule of the invention

SQ Sequence 772 AA;

#### Alignment Scores:

Pred. No.: 3,4e-137 Length: 772  
 Score: 1732.50 Matches: 335  
 Percent Similarity: 70.58% Conservative: 44  
 Best Local Similarity: 62.38% Mismatches: 79  
 Query Match: 64.29% Indels: 79  
 DB: 4 Gaps: 8

US-10-048-116-1 (1-1484) x ABB56463 (1-772)

QY	64	GGAGGT-----GAAGACGACATTGAGCGCGACACGCTAGGCTTCATGCTACAAC	114
DB	250	GlyGlySerSerSerGluAspAspIleGluAlaAspHisValGlyValTyrGlyThr	269
QY	115	GTTTATCAGTCTCTCGAGACATTGGCCAGTACACATGAATTTGATGCTGATGAGTTG	174
DB	270	ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyr	289
QY	175	TTCTATGTGACTTGTGATAGAGAAAGAACTGCTCGAGGCTTCCTGAGTTTGCCCAATG	234
DB	290	PheTyrValAspLeuAspLysGlyGluThrIleTyrMetLeuProGluPheGlyGlnLeu	309
QY	235	ATACTCTTTCAGCCCAAGGTGACTGCAAAACATAGCTGCAGAAAACACACTTTGGGA	294
DB	310	ThrSerPheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly	329
QY	295	ATCTTGACTAAGAGGTCAAAATTTCAACCCAGCTACCAATGAGGCTCTCAAGGACTGTG	354
DB	330	IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal	349
QY	355	TTCCCAAGTCCCTGTGCTGGGTGAGCCCAACACCTTATCTGCTTTTGTGGCAAC	414
DB	350	PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn	369
QY	415	ATCTTCCCACTGTGATCAACATCAGTGGCTCAGAAATAGCAAGTCAGTCACAGCGGC	474
DB	370	IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly	389
QY	475	GTTTATGAGACACAGCTCTCTCGTCAACCGTGACCATTTCTTCACAAAGCTGTCTATCTC	534
DB	390	ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu	409
QY	535	ACCTTCATCCCTTCTGATGATACATTTATGATGCAAGGTGAGCACTGGGCGCTGGAG	594
DB	410	ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTyrGlyLeuGlu	429
QY	595	GAGCCGGTCTTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGCAGAA	654
DB	430	GluProValLeuLysHisTyr-----A1a 437	
QY	655	ACTGGAGGTGGAGATCC-----ACTACAGCTCCATCA-----687	
DB	438	SerGlyGlyGlySerGlyGlySerLeuAlaLysThrThrProSerValTyr 457	
QY	687	-----687	
DB	458	ProLeuAlaProGlySerAlaAlaGlnThrAsnSerMetValThrLeuGlyCysLeuVal 477	
QY	687	-----687	
DB	478	LysGlyTyrPheProGluProValThrValThrTrpAsnSerGlySerLeuSerSerGly 497	
QY	688	-----GCTCAGCTCGAAAAAGAGCTCCAGCGCTCGAGAGGAATGCA 732	
DB	498	ValHisThrPheProAlaValLeuGlnSerAspLeuTyrThrLeuSerSerValThr 517	
QY	733	-----CAGTGGAAATGGGAGTTGCAAGCACTGGAAAGAACTGGCTCAGCGCATCT 786	

DB	518	ValProSerSerThrTrpProSerGluThrValThrCysAsnValAlaHisProAlaSer	537
QY	787	GAGCCCCAGA---GGGCCCACAATCAAGCCC-----TGCTCTCCATCAATGC	831
DB	538	SerThrLysValAspLysLysIleValProArgAspCysGlyCysLysProCysIleCys	557
QY	832	CCAGCACCTTAACCTCTTGGGTGGACCATCCGCTTCATCTTCCTCCCAAGATCAAGGAT	891
DB	558	ThrValProGluVal-----SerSerValPheIlePheProLysProLysAsp	574
QY	892	GTAATCATGATCTCCCTGAGCCCATAGTACATGTGTGGTGTGTGATGACGAGGAT	951
DB	575	ValLeuThrIleThrLeuThrProLysValThrCysValValAspIleSerLysAsp	594
QY	952	GACCCAGATGTCAGATCAGCTGGTTGTGAACAACGTCGAACTCACACAGCTCAGACA	1011
DB	595	AspProGluValGlnPheSerTrpPheValAspAspValGluValHisThrAlaGlnThr	614
QY	1012	CAAACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCTCCCATCCAG	1071
DB	615	GlnProArgGluGluGlnPheAsnSerThrPheArgSerValSerGluLeuProIleMet	634
QY	1072	CACCAGGACTGATGATGCGCAAGGAGTTCAATGCAAGGTCAACAACAAGACCTCCCA	1131
DB	635	HisGlnAspTrpLeuAsnGlyLysGluPheLysCysArgValAsnSerAlaAlaPhePro	654
QY	1132	GGCCCATCGAGAGACCATCTCAAAACCCAAAGGTCAGTAAGAGCTCCACAGGTATAT	1191
DB	655	AlaProIleGluLysThrIleSerLysThrLysGlyArgProLysAlaProGlnValTyr	674
QY	1192	GTCCTGCTCCACCAAGAAGAGATGACTAAAGAAACAGGTCACTCTGACCTGCATGGTC	1251
DB	675	ThrIleProProLysGluGlnMetAlaLysAspLysValSerLeuThrCysMetIle	694
QY	1252	ACAGACTTCATGCTGAGACATTTACGTGGAGTGGACCAACAACGGGAAAAACAGACTA	1311
DB	695	ThrAspPhePheProGluAspIleThrValGluTrpGlnTrpAsnGlyGlnProAlaGlu	714
QY	1312	AACTCAACAACACTGAACAGTCCTGGAGCTCTGATGGTTCTTACTTCATGTCACAGCAAG	1371
DB	715	AsnTyrLysAsnThrGlnProIleMetAspThrAspGlySerTyrPheValTyrSerLys	734
QY	1372	CTGAGAGTGGAAAAAGAACTGGGTGGAAAGAAATAGTACTCTCTGTCAGTGGTCCAC	1431
DB	735	LeuAsnValGlnLysSerAsnTrpGluAlaGlyAsnThrPheThrCysSerValLeuHis	754
QY	1432	GAGGCTCTGCACAATCACACAGACTAAGAGCTTCCTCCGGAGCTCCGGGT 1482	
DB	755	GluGlyLeuHisAsnHisThrGluLysSerLeuSerHisSerProGly 771	

#### RESULT 6

ABB56458 ID ABB56458 standard; protein; 676 AA.

AC ABB56458;

XX 25-FEB-2002 (first entry)

DE 1AS MBP 1-14 CH1.H protein.

XX Mouse; MHC; major histocompatibility complex; MHC class II; multimer;  
 single chain; immunosuppressive; antidiabetic; antiinflammatory;  
 antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;  
 autoimmune disease; insulin dependent diabetes; multiple sclerosis;  
 myaesthesia gravis; pernicious anaemia; autoimmune encephalomyelitis;  
 rheumatoid arthritis; systemic lupus erythematosus.

OS Mus sp.

OS Synthetic.

XX WO200170245-A1.

XX 27-SEP-2001.

PD



XX 22-MAR-2001; 2001WO-US009616.  
 XX PF  
 XX PR  
 XX PR 22-MAR-2000; 2000US-0191274P.  
 PR 15-MAY-2000; 2000US-0204249P.  
 PR 23-JAN-2001; 2001US-0264003P.  
 XX PR  
 XX (CORI-) CORIXA CORP.  
 PA  
 XX Carter D, Zhu S, Arimilli S, Wang A;  
 PI  
 XX WPI; 2001-616371/71.  
 DR N-PSDB; AS199028.  
 DR  
 XX Multimeric complex for treating autoimmune diseases, comprises first and  
 PT second single chain MHC class II molecules, each comprising alaphal and  
 PT beta1 domain linked through amino acid linker and multimerization domain.  
 XX  
 XX Example 7; Page 99-101; 147pp; English.  
 PS  
 XX The invention relates to a multimeric complex comprising a first  
 CC recombinant single chain major histocompatibility complex (MHC) class II  
 CC molecule and a second recombinant single chain MHC class II molecule,  
 CC each comprising an alaphal domain and a beta1 domain linked through an  
 CC amino acid linker and a multimerization domain. The first and the second  
 CC molecule are linked through the multimerization domain to form a  
 CC multimeric complex. The complex is useful for treating autoimmune  
 CC diseases. It is useful for treating insulin dependent diabetes, multiple  
 CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune  
 CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus  
 CC erythematosus. The present sequence is a single chain MHC class II  
 CC molecule of the invention  
 XX  
 SQ Sequence 676 AA;

Alignment Scores:  
 Pred. No.: 2,396-119 Length: 676  
 Score: 1521.00 Matches: 304  
 Percent Similarity: 71.98% Conservative: 12  
 Best Local Similarity: 69.25% Mismatches: 39  
 Query Match: 56.44% Indels: 84  
 DB: 4 Gaps: 8

US-10-048-116-1 (1-1484) x ABB56458 (1-676)

QY 64 GGAGT-----GAAGACGACATTGAGCCGACACCGTAGGCTTCTATGTGTAACA 114  
 DB 250 GlyGlySerSerSerGluAspIleGluAlaAspHisValGlyValTyrGlyThrThr 269  
 QY 115 GTTTATCATGCTCTCTGGAGACATTGGCCAGTACACACATGATTTGATGGTGTGAGTTG 174  
 DB 270 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTrp 289  
 QY 175 TTCTATGTGGACTTGGTAAGAGAAACTCTCTGGAGGCTCTCTGAGTTTGGCAATTG 234  
 DB 290 PheTyrValAspLeuAspLysGlyGlnThrIleTrpMetLeuProGluPheGlyGlnLeu 309  
 QY 235 ATACTCTTTGAGCCCCAGGTGGAGTGCAGAACATAGTGTGAGAAAAACAACTTGGGA 294  
 DB 310 ThrSerPheAspProGlnGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly 329  
 QY 295 ATCTTGACTAAGAGTCAAAATTCACCCAGCTACCAATGAGGCTCTCAAGGACTGTG 354  
 DB 330 IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal 349  
 QY 355 TTCCCCAGTCCCTGTGCTGCTGGTCAGCCCAACACCTTATCTGCTTGTGTGCAAC 414  
 DB 350 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 369  
 QY 415 ATCTTCCACCTGTGATCAACATCACATGGCTGAGAAATAGCAAGTCAGTCACAGCGGC 474  
 DB 370 IlePheProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 389

QY 475 GTTTATGAGACCGACTTCTCGTCAACCGTGACCAATTCCTTCCACAAGCTGTCTTATCTC 534  
 DB 390 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 409  
 QY 535 ACCTTCATCCTCTCTGATGATGACATTATGACTGCAAGGTGGAGCACTGGGGCTCGAG 594  
 DB 410 ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 429  
 QY 595 GAGCCGGTCTTGAACACACTGGGAACCTGAGATTCCAGCCCCCATGTGTCAGAGCTGACAGAA 654  
 DB 430 GluProValLeuLysHisTrp-----Ala 437  
 QY 655 ACTGGAGGTGAGGATCC-----ACTACAGCTCCATCA- 687  
 DB 438 SerGlyGlyGlySerGlyGlyGlyAlaLysThrProProSerValTyrPro 457  
 QY 687 ----- 687  
 DB 458 LeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLys 477  
 QY 687 ----- 687  
 DB 478 GlyTyrPheProGluSerValThrValThrTrpAsnSerGlySerLeuSerSerVal 497  
 QY 688 -----GCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAATGCA--- 732  
 DB 498 HisThrPheProAlaLeuGlnSerGlyLeuTyrThrMetSerSerValThrVal 517  
 QY 733 ---CAGCTGGAATGGGAGTTGCAAGCACTGMAAGGAACCTGGCTCAGCGAGCATCT--- 786  
 DB 518 ProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHisProAlaSerSer 537  
 QY 787 -----GAGCCGAGGGGCC-----ACAATCAAGCCCTGTCTCT 819  
 DB 538 ThrThrValAspLysLysLeuGluProSerGlyProIleSerThrIleAsnProCysPro 557  
 QY 820 CCATGC-----AAATGCCAGCAGCCTTAACCTCTGGTGGACCATCTCGTCTTC 867  
 DB 558 ProCysLysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPhe 577  
 QY 868 ATCTTCTCCTCAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGT 927  
 DB 578 IlePheProProAsnIleLysAspValLeuMetIleSerLeuThrProLysValThrCys 597  
 QY 928 GTGTGTGTGATGTGACGAGGATGACCCAGATGTCCAGATCAGCTGCTTTGTGAACAAC 987  
 DB 598 ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn 617  
 QY 988 GTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACACAGTACTCTCGG 1047  
 DB 618 ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArg 637  
 QY 1048 GTGTGTGAGTGCCTCCCTCCAGCAGCAGCAGTGGATGAGTGGCAAGGAGTTCAAAATGC 1107  
 DB 638 ValValSerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys 657  
 QY 1108 AAGTCAACAAACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAA 1164  
 DB 658 LysValAsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLys 676

RESULT 7

ABB56457  
 ID ABB56457 standard; protein; 678 AA.

XX AC ABB56457;  
 XX AC

XX 25-FEB-2002 (first entry)  
 XX DT

XX IAS MBP 1-14 CH1.H.CH2.CH3 protein.  
 XX DE

XX Mouse; MHC; major histocompatibility complex; MHC class II; multimer;  
 KW single chain; immunosuppressive; antidiabetic; antiinflammatory;  
 KW antianaemic; antirheumatoid; antiarthritic; neuroprotective; vaccine;

KW autoimmune disease; insulin dependent diabetes; multiple sclerosis;  
 KW myasthenia gravis; pernicious anaemia; autoimmune encephalomyelitis;  
 KW rheumatoid arthritis; systemic lupus erythematosus.

OS Mus sp.  
 OS Synthetic.

XX WO200170245-A1.

XX 27-SEP-2001.

XX 22-MAR-2001; 2001WO-US009616.

XX 22-MAR-2000; 2000US-0191274P.

PR 15-MAY-2000; 2000US-0204249P.

PR 23-JAN-2001; 2001US-0264003P.

PA (CORI-) CORIXA CORP.

XX Carter D, Zhu S, Arimilli S, Wang A;

XX WPI; 2001-616371/71.

DR N-PSDB; ABI99027.

XX Multimeric complex for treating autoimmune diseases, comprises first and

PT second single chain MHC class II molecules, each comprising alpha1 and

PT beta1 domain linked through amino acid linker and multimerization domain.

XX Example 7; Page 96-98; 147pp; English.

XX The invention relates to a multimeric complex comprising a first  
 CC recombinant single chain major histocompatibility complex (MHC) class II  
 CC molecule and a second recombinant single chain MHC class II molecule,  
 CC each comprising an alpha1 domain and a beta1 domain linked through an  
 CC amino acid linker and a multimerization domain. The first and the second  
 CC molecule are linked through the multimerization domain to form a  
 CC multimeric complex. The complex is useful for treating autoimmune  
 CC diseases. It is useful for treating insulin dependent diabetes, multiple  
 CC sclerosis, myasthenia gravis, pernicious anaemia, autoimmune  
 CC encephalomyelitis (EAE), rheumatoid arthritis and systemic lupus  
 CC erythematosus. The present sequence is a single chain MHC class II  
 CC molecule of the invention

XX Sequence 678 AA;

Alignment Scores:

Pred. No.: 2.39e-119 Length: 678  
 Score: 1521.00 Matches: 304  
 Percent Similarity: 71.98% Conservative: 12  
 Best Local Similarity: 69.25% Mismatches: 39  
 Query Match: 56.44% Indels: 84  
 DB: 4 Gaps: 8

US-10-048-116-1 (1-1484) x ABB56457 (1-678)

QY 64 GGAGGT-----GAAGACGACATTGAGGCGCACCGTAGGCTTCTATGTACAACT 114  
 DB 252 GLVGLYSerSerSerGluAspAspIleGluAlaAspHisValGlyValTyrGlyThrThr 271  
 QY 115 GTTTATCAGTCTCTGAGACATTGGCCAGTACACATCAATTTGATGGTGTGATGTTG 174  
 DB 272 ValTyrGlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyr 291  
 QY 175 TTCTATGTGACATTGNTAGAGAAAACATGCTTGGAGGCTTCTGAGTTTGGCCAAATG 234  
 DB 292 PheTyrValAspLeuAspLysLysGluThrIleTyrMetLeuProGluPheGlyGlnLeu 311  
 QY 235 ATACTCTTTCAGCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAACACAACTTTGGGA 294  
 DB 312 ThrSerPheAspProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGly 331  
 QY 295 ATCTTGACTAAGAGGTCAAAATTTTCAACCCAGCTACCAATGAGGCTCTCTCAAGCGACTGTG 354

RESULT 8  
 ADL15170  
 ID ADL15170 standard; protein; 426 AA.

Db 332 IleLeuThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrVal 351  
 QY 355 TTTCCCAAGTCCCTCTGCTGCTGGGTGAGCCCAACACACCTTATCTGCTTTGGACAAC 414  
 Db 352 PheProLysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsn 371  
 QY 415 ATCTTCCCACTGTGTATCAACATCAGTGGCTCAGAAATAGCAAGTCAAGTCAAGCGGC 474  
 Db 372 IlePheProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGly 391  
 QY 475 GTTTATGAGACGAGCTTCTCTGTCACACCTGACCATCTCTTCCACAGCTGTCTTATCTC 534  
 Db 392 ValTyrGluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeu 411  
 QY 535 ACCTTCATCCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 594  
 Db 412 ThrPheIleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGlu 431  
 QY 595 GAGCCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCTCAGAGCTGACAGAA 654  
 Db 432 GluProValLeuLysHisTrp-----Ala 439  
 QY 655 ACTGAGGTGGAGGATCC-----ACTACAGCTCATCA-----687  
 Db 440 SerGlyGlyGlyGlySerGlyGlyGlyAlaLysThrThrProProSerValTyrPro 459  
 QY 687 -----687  
 Db 460 LeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLys 479  
 QY 687 -----687  
 Db 480 GlyTyrPheProGluSerValThrValThrTrpAsnSerGlySerLeuSerSerVal 499  
 QY 688 -----GCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAATGCA---732  
 Db 500 HisThrPheProAlaLeuLeuGlnSerGlyLeuTyrThrMetSerSerValThrVal 519  
 QY 733 ---CAGCTGGATGGAGTGGCAAGCACTGGAAGAACTGCTCAGGCGAGCATCT---786  
 Db 520 ProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHisProAlaSerSer 539  
 QY 787 -----GAGCCCGAGAGGCGCC-----ACAATCAAGCCCTGTCTCT 819  
 Db 540 ThrThrValAspLysLysLeuGluProSerGlyProIleSerThrIleAsnProCysPro 559  
 QY 820 CATGC-----AAATGCCCGAGCACCTTAACCTCTTGGGTGGAGCATCCGTCTTC 867  
 Db 560 ProCysLysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPhe 579  
 QY 868 ATCTTCCCTCCAAAGATCAAGGATGACTCATGATCTCCCTGAGCCCCATAGTCACATGT 927  
 Db 580 IlePheProProAsnIleLysAspValLeuMetIleSerLeuThrProLysValThrCys 599  
 QY 928 GTGGTGGTGGATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTGTGTGAACAAC 987  
 Db 600 ValValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsn 619  
 QY 988 GTGGAAGTACACAGCTCAGACACAAACCCATAGAGAGATTACACAGTACTCTCCGG 1047  
 Db 620 ValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArg 639  
 QY 1048 GTGGTCAGTGCCTCCCATCCAGCACAGGATGATGATGATGATGATGATGATGATGATG 1107  
 Db 640 ValValSerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCys 659  
 QY 1108 AAGGTCAACAAAGAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCCAA 1164  
 Db 660 LysValAsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLys 678

```

XX AC ADL15170;
XX DT 06-MAY-2004 (first entry)
XX DE Murine modified S antibody (S-Ab) protein.
XX KW Modified S immunoglobulin antibody; constant region; immunoglobulin; Ig;
XX KW IgG2a; modified S antibody; S-Ab; immune disorder; infectious disorder;
XX KW cancerous disorder; murine; antirheumatic; antiarthritic; osteopathic;
XX KW antiinflammatory; dermatological; immunosuppressive; ophthalmological;
XX KW antibacterial; virucide; anti-HIV; vasotropic; antiallergic;
XX KW hepatotropic.
XX OS Mus sp.
XX PN US2003232046-A1.
XX PD 18-DEC-2003.
XX PF 05-JUN-2003; 2003US-00454948.
XX PR 14-JUN-2002; 2002US-0388896P.
XX PA (SCAL/) SCALLON B J.
XX PA (CAIA/) CAI A.
XX PA (NASO/) NASO M.
XX PI Scallion BJ, Cai A, Naso M;
XX DR WPI; 2004-052145/05.
XX PT Modified S immunoglobulin molecule useful for treating immune disorder or
XX PT diseases especially immune conditions e.g. rheumatoid arthritis,
XX PT osteoarthritis, inflammatory bowel disease or systemic lupus
XX PT erythematosus.
XX PS Example 1; SEQ ID NO 2; 37pp; English.
XX CC The present invention relates to modified "s" immunoglobulin antibodies
XX CC that have an extra constant region immunoglobulin (Ig) domain inserted
XX CC into the constant region of the Ig molecule. Preferably, the extra
XX CC constant region Ig domain comprises a CH3, CH1 or CH2 domain, and the Ig
XX CC molecule is IgG1, where the extra constant region Ig domain comprises a
XX CC CH1 domain of an IgG2a immunoglobulin. The modified "s" antibody (S-Ab)
XX CC is useful for treating immune disorders (e.g. rheumatoid
XX CC arthritis/seronegative arthropathies, osteoarthritis, inflammatory bowel
XX CC disease, systemic lupus erythematosus, iridocyclitis/uveitis/optic
XX CC neuritis, idiopathic pulmonary fibrosis, systemic vasculitis/wegener's
XX CC granulomatosis), and infectious or cancerous disorders (e.g. chronic
XX CC bacterial infection, acute and chronic parasitic or infectious processes,
XX CC including bacterial, viral and fungal infections, HIV infection/HIV
XX CC neuropathy, meningitis, hepatitis, septic arthritis, peritonitis,
XX CC pneumonia, epiglottitis). The present sequence represents a murine S-Ab
XX CC protein.
XX SQ Sequence 426 AA;

Alignment Scores:
Pred. No.: 5e-103 Length: 426
Score: 1327.00 Matches: 264
Percent Similarity: 70.15% Conservative: 25
Best Local Similarity: 64.08% Mismatches: 49
Query Match: 49.24% Indels: 74
DB: 8 Gaps: 7

US-10-048-116-1 (1-1484) x ADL15170 (1-426)
QY 265 AACATAGTCGAGAAAACACAACTGGGAATCTTGACTAGAGGTCAAAATTCACCCCA 324
Db |||||
82 AsnValAlaHisProAlaSerThrLysValAspLysLysIleAlaLysThrPro 101
QY 325 GCTACCAATGAGGCTCCTCAAGCAGCTGTGTTCCCAAGTCCCTCTGCTCTGGGTGAG 384

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Db 394 LysAsnTrpValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsn 413

QY 1447 CACCACAGACTAAGAGCTTCTCCGAGACTCCGGGT 1482

Db 414 HisHisThrThrLysSerPheSerArgThrProGly 425

RESULT 9

AA40384

ID AAR40384 standard; protein; 469 AA.

XX AAR40384;

XX 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 08-FEB-1994 (first entry)

XX Monoclonal antibody M(alpha)2-3 Heavy-chain.

XX anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin;

KW bispecific bivalent antibody; cell-targeting; cytotoxic agent.

XX Unidentified.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Region /label= signal\_peptide

FT Region 20..139

FT Region /label= variable

FT Region 140..236

FT Region /label= constant

FT Region 237..252

FT Region /label= joining

FT Region 253..362

FT Region /label= constant

FT Region 363..469

FT Region /label= constant

XX EP556111-A1.

PN 18-AUG-1993.

PD 09-FEB-1993; 93BP-00400323.

PF 11-FEB-1992; 92FR-00001505.

PR (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PA Boulain J, Ducancel F, Gillet D, Menez A;

PI WPI; 1993-260351/33.

XX N-PSDB; AAQ48037.

DR New immunoglobulin hybrid proteins - with immunoglobulin fragments linked

DR to dimeric protein, for diagnostic or therapeutic use.

XX Example 1; Fig 3A; 37pp; French.

XX A fragment of the heavy chain (VH + CH1) from the anti-snake small

CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from

CC hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain

CC fragment (VL + CL) was amplified from the same source using primers

CC AAQ48041 and AAQ48042. The two amplified fragments were inserted into the

CC same vector; the H-chain fragment was inserted (in-frame) between codons

CC 6-7 of the phoA coding sequence and the L-chain fragment was inserted

CC into a cassette which contained a phoA S-D sequence, a signal peptide and

CC the first 6 codons of phoA. The cassette was positioned between the

CC termination codon and the transcription termination sequence of phoA. The

CC fusion construct is expected to encode a hybrid protein comprising two

CC identical Ab-derived units. The invention also covers hybrid proteins

CC containing two different Ab-derived units (i.e. to produce bispecific

CC antibodies). When a toxic protein is used in place of phoA, the hybrid

CC molecules can be used as cell-targeting therapeutic agents. (Updated on

CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct

CC PN field.)

XX SQ Sequence 469 AA;

Alignment Scores:

Pred. No.: 2,22e-102 Length: 469

Score: 1319.50 Matches: 283

Percent Similarity: 60.96% Conservative: 23

Best Local Similarity: 56.37% Mismatches: 71

Query Match: 48.96% Indels: 125

DB: 2 Gaps: 13

US-10-048-116-1 (1-1484) x AAR40384 (1-469)

QY 100 TTCTATGGTACAACTGTTTATCAGTCTCTCTGGAGAC-----ATTGCG----- 141

Db 51 TyrTyrIleAsnTrpValLysGlnLysProGlyGlnGlyLeuLysTrpIleGlyTrpIle 70

QY 142 -----CAGTACACACATGAATTTGATGGTGATGAGTTGTTCTAT 180

Db 71 TyrProAlaSerGlyAsnThrLysTyrAsnGluAsnPheLysGlyLysAlaThrLeuThr 90

QY 181 GTGGACTTCGATAAGAGAAACTGTCTGGAGGCTTCCTGAGTTT----- 225

Db 91 ValAspThrSerSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSerGluAspThr 110

QY 226 -----GGCCAAATTGATCTCTTTGAGCCC 249

Db 111 AlaValTyrPheCysAlaArgAlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGly 130

QY 250 CAAGTGGAGTCGAAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTGACTAAGAGG 309

Db 131 GlnGlyThrThrLeuThrValSerSerAlaLys----- 141

QY 310 TCMAATTTCCACCCAGCTACCAATGAGGCTCTCAAGCCAGCTGTGTTCCTCCCAAGTCCCT 369

Db 142 -----ThrThrAlaPro-----SerValTyrProLeuAlaPro 152

QY 370 GTG-----CTGCTGGTCAAGCCAAACACCTTATCTGCTTTTGTGACAAACATCTTC 420

Db 153 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 172

QY 421 CCACCTGTGATCAACATCATGGTTCAGAAATAGCAAGTCAGTCACAGACGCGTTTAT 480

Db 173 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 189

QY 481 GAGACAGCTTCTCTGTCACACCGTGACCATTCCTCCACAGCTGTCTTATCTCACCTTC 540

Db 190 -----HisThrPheProAlaVal----- 195

QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGAGAGCCG 600

Db 196 -----LeuGlnSerAspLeuTyrThrLeuSer----- 204

QY 601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAAACTGGA 660

Db 205 -----SerSerValThrValThr--- 210

QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGTCCGAAAAAGAGAGCTCCAGGCCCTGGAG 720

Db 211 -----SerSerThr----- 213

QY 721 AAGGAAATGTCACAGCTGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA 780

Db 214 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 226

QY 781 GCATCT-----GAGCCCAAGGGCCCAACAATCAAGCCCTGT 816

Db 227 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 246

QY 817 CTTCATGCAAAATGCCAGACACTAACCTCTTGGGTGGAGCCATCCGCTCTTCATCTCCCT 876

Db 247 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 266



```
QY 877 CCAAAGATCAAGGATGATCTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTG 936
Db 266 ProlysisLeuAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 285
QY 937 GATGTGAGCGAGGATGACCCAGATGTCTCAGATCAGCTGGTTTGTGAACACGTGGAGTA 996
Db 286 AspValSerGluAspAepProAspValGlnIleSerTrpPheValAsnAenValGluVal 305
QY 997 CACACAGCTCAGACACAAACCCATAGAGAGATTTACAAACAGTACTCTCCGGGTGGTCAGT 1056
Db 306 HisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer 325
QY 1057 GCCCTCCCATCCAGCACACAGAGCTGATGAGTGGCAAGAGTTCAAATCAAGGTCAAC 1116
Db 326 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 345
QY 1117 AACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA 1176
Db 346 AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 365
QY 1177 GCTCCACAGGTATATGTCTTGGCTCCACACAGAGAGATGACTAAGAAACAGGTCACT 1236
Db 366 AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr 385
QY 1237 CTGACCTGTCATGTCACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAAC 1296
Db 386 LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn 405
QY 1297 GGGAAACAGAGCTAACTACAGAACACTGAACCACTGCTGACCTGTGATGTTCTTAC 1356
Db 406 GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr 425
QY 1357 TTCATGTACAGCAAGCTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTCTCC 1416
Db 426 PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer 445
QY 1417 TGTTCAGTGTCCACGAGGTCTGCACAATCACCACACGACTAAGAGCTTCTCCCGGACT 1476
Db 446 CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThr 465
QY 1477 CCGGGT 1482
Db 466 ProGly 467

RESULT 11
ADQ91057
ID ADQ91057 standard; peptide; 468 AA.
AC ADQ91057;
DT
DT 23-SEP-2004 (first entry)
XX
DE Murine OKT3 antibody heavy chain SEQ ID NO:38.
XX
KW CDR3; antiinflammatory; antimicrobial; cytostatic; immunomodulator;
KW immunosuppressive; proliferative disease; tumour; inflammatory disease;
KW immunological disorder; autoimmune disease; infectious disease; OKT3;
KW heavy chain; antibody.
XX
OS Mus sp.
XX
XX CA2403313-A1.
XX
PD 11-APR-2004.
XX
XX 11-OCT-2002; 2002CA-02403313.
XX
PR 11-OCT-2002; 2002CA-02403313.
XX
PA (MICR-) MICROMET AG.
XX
PI Lanzavecchia A;
XX
```

```
DR WPI; 2004-390792/37.
DR N-PSDB; ADQ91058.
XX
PT Antibody construct, useful in treating, e.g., cancer and inflammatory
PT diseases comprises at least one mutated CDR3 region.
XX
XX Example 1; SEQ ID NO 38; 80pp; English.
XX
The invention relates to a novel polypeptide construct comprising at
CC least one CDR3 region comprising at least one mutation in a fully defined
CC sequence of 6 amino acids. A construct of the invention has
CC antiinflammatory, antimicrobial, cytostatic, immunomodulator, and
CC immunosuppressive activity. The polypeptide construct, polynucleotide,
CC vector or composition are useful for the prevention, treatment or
CC amelioration of a proliferative disease, a tumorous disease, an
CC inflammatory disease, an immunological disorder, an autoimmune disease or
CC an infectious disease in a human subject. The present sequence represents
CC the OKT3 antibody heavy chain.
XX
SQ Sequence 468 AA;

Alignment Scores:
Pred. No.: 7,13e-102 Length: 468
Score: 1313.50 Matches: 265
Percent Similarity: 70.65% Conservative: 19
Best Local Similarity: 65.92% Mismatches: 41
Query Match: 48.74% Indels: 77
DB: 8 Gaps: 8

US-10-048-116-1 (1-1484) x ADQ91057 (1-468)
QY 310 TCAAAATTTCCACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTCCCAAGTCCCT 369
Db 132 ThrThrLeuThrValSerSerAlaLysThrThrAlaProSerValTyrProLeuAlaPro 151
QY 370 GTG-----CTGCTGGGTGAGCCCAACACCCCTTATCTGTCTTGTGACAAACATCTTC 420
Db 152 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 171
QY 421 CCACCTGTGATCAACATCAGATGGCTCAGAAATAGCAAGTACGTCACAGACGGCTTAT 480
Db 172 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerGlyVal--- 188
QY 481 GAGACGAGCTTCTCTGTCACCGTGACCATCTCTCCACAAGCTGTCTTATCTCACCTTC 540
Db 189 -----HisThrPheProAlaVal----- 194
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCCG 600
Db 195 -----LeuGlnSerAspLeuTyrThrLeuSer----- 203
QY 601 GTTCTGAACACTGGGAACCTGAGATTCAGCCCCCATGTCTCAGAGCTGACAGAACTGGA 660
Db 204 -----SerSerValThrValThr--- 209
QY 661 GTGGAGGATCCATACAGCTCCATCAGCTCAGCTCGAATAAGAGCTCCAGGCCCTGGAG 720
Db 210 -----SerSerThr----- 212
QY 721 AAGGAAATGCACAGCTGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA 780
Db 213 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 225
QY 781 GCATCT-----GAGCCAGAGGGCCCAATCAAGCCCTGT 816
Db 226 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 245
QY 817 CCTCCATGCAAAATGCCAGCAGCTAACCTCTTGGGTGGACCATCCGCTCTTCATCTCCCT 876
Db 246 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 265
QY 877 CCAAAGATCAAGGATGATCTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTG 936
Db
```

Db 266 ProlysinLeuAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 285  
Qy 937 GATGTGACGAGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACGTCGAAGTA 996  
Db 286 AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal 305  
Qy 997 CACACAGCTCAGACACAAACCATAGAGAGATTACACAGTACTCTCCGGTGGTCAGT 1056  
Db 306 HistHrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer 325  
Qy 1057 GCCCTCCCATCCAGCACAGACTGGATGATGGCAAGGAGTTCAAATGCAAGTCAAC 1116  
Db 326 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 345  
Qy 1117 AACAAAGACCTCCAGGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA 1176  
Db 346 AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 365  
Qy 1177 GCTCCACAGGTATATGCTTGCCTCCACCAAGAGAGATGACTAAGAACAGGTCACT 1236  
Db 366 AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr 385  
Qy 1237 CTGACCTGTCATGGTCACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAC 1296  
Db 386 LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn 405  
Qy 1297 GGGAAACAGAGCTAAACTACAAGAACACTGAACAGTCTGGACTCTGATGGTCTTAC 1356  
Db 406 GlyLysThrGluLeuAsnTyr-LysAsnThrGluProValLeuAspSerAspGlySerTyr 425  
Qy 1357 TTCATGTACAGACAGCTGAGAGTGGAAAGAGAGACTGGGTGGAAAGAAATAGTACTCC 1416  
Db 426 PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer 445  
Qy 1417 TGTTCAGTGGTCCACGAGGGTCTGCACAATCACACAGACTAAGAGCTTCTCCCGGACT 1476  
Db 446 CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThr 465  
Qy 1477 CCGGGT 1482  
Db 466 ProGly 467  
RESULT 12  
ADL15695  
ID ADL15695 standard; protein; 329 AA.  
AC ADL15695;  
XX  
DT 20-MAY-2004 (first entry)  
DE Murine immunoglobulin heavy chain constant region protein SeqID 69.  
XX  
XX mouse; murine; antibody; beta-amyloid; A-beta;  
KW amyloid beta A4 precursor protein; APP; presenilin;  
KW lipoprotein receptor related protein; LRP; beta-amyloid 42; A-beta 42;  
KW Alzheimer's disease; neuroprotective; nontropic.  
XX  
OS Mus musculus.  
XX  
XX WO2004018997-A2.  
XX  
XX 04-MAR-2004.  
XX  
XX 20-AUG-2003; 2003WO-US026173.  
XX  
XX 20-AUG-2002; 2002US-0405417P.  
XX  
XX 18-SEP-2002; 2002US-0411974P.  
XX  
XX (NEUR-) NEUROGENETICS INC.  
XX  
XX Kounnas M, Patrick A, Velicelebi G, Wagner S;  
XX WPI; 2004-226902/21.  
DR

DR N-PSDB; ADL15694.  
XX  
PT New polypeptide comprises a sequence of amino acids that is selectively  
PT reactive with beta-amyloid peptide 42 or at least one complementarity-  
PT determining region of antibody A387 or B436, useful for treating  
PT Alzheimer's disease.  
XX  
PS Claim 35; SEQ ID NO 69; 408pp; English.  
XX  
CC This invention relates to novel methods and compositions for detecting  
CC and modulating beta-amyloid (A-beta) peptide levels and the processing of  
CC amyloid beta A4 precursor protein (APP). Specifically, it refers to  
CC methods of assessing the presenilin activity of compounds using the  
CC lipoprotein receptor related protein (LRP), in order to identify  
CC presenilin proteins that can be used to affect the processing of APP. The  
CC present invention describes methods to identify agents that modulate  
CC presenilin activity and A-beta levels, in particular beta-amyloid 42 (A-  
CC beta 42), such that the agent is selectively reactive with A-beta 42 and  
CC binds at least one complementarity determining region (CDR) of either  
CC antibody A387 or antibody B436. As such, the polypeptides, nucleic acids  
CC and antibodies are useful for treating Alzheimer's disease, accordingly  
CC the compositions exhibit neuroprotective and nontropic activities. This  
CC peptide sequence is a murine antibody chain peptide of the invention.  
XX  
SQ Sequence 329 AA;  
Alignment Scores:  
Pred. No.: 9.37e-102 Length: 329  
Score: 1311.50 Matches: 264  
Percent Similarity: 71.72% Conservative: 15  
Best Local Similarity: 67.87% Mismatches: 33  
Query Match: 48.66% Indels: 77  
DB: 8 Gaps: 8  
US-10-048-116-1 (1-1484) x ADL15695 (1-329)  
Qy 349 ACTGTGTTCCTCCCAAGTCCCTGTG-----CTGCTGGTTCAGCCCAACACCTTATC 399  
Db 6 SerValTyrProLeuAlaProValCysGlyAspThrThrGlySerSerValThrLeuGly 25  
Qy 400 TGCTTTGTGGACACATCTTCCCACTGTGATCAACATCATCATGGCTCAGAAATAGCAAG 459  
Db 26 CysLeuValLysGlyTyrPheProGluProValThrLeuThrTrp-----AsnSerGly 43  
Qy 460 TCAGTCAACAGACGGCGTTTATGAGACCCAGCTTCTCTCAACCGTAGCACTTCTTCCAC 519  
Db 44 SerLeuSerSerGlyVal-----HisThrPhePro 53  
Qy 520 AAGCTGTCTTATCTCACCTTCTCATCCCTTCTGTATGATGACATTTATGACTGCAGGTGGAG 579  
Db 54 AlaVal-----LeuGlnSerAspLeuTyrThrLeuSer----- 64  
Qy 580 CACTGGGGCTGGAGGAGCGGTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATG 639  
Db 64 ----- 64  
Qy 640 TCAGAGCTGACAGAAACTGGAGGTGGAGATTCACATACAGCTCCATCAGCTCAGCTCGAA 699  
Db 65 SerSerValThrValThr-----SerSerThr----- 73  
Qy 700 AAGAGCTCCAGGCCCTGGAGAGAGAAATGCACAGCTGGGAATGGGAGTTGCAAGCACTG 759  
Db 74 -----TrpProSerGlnSerile 79  
Qy 760 GAAAGGAAGTGGCTCAGGCAGCATCT-----GAGCCCAAGA 795  
Db 80 ThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGluProArg 99  
Qy 796 GGGCCCACAATCAAGCCCTCTCTCCATGCAATGCAATGCAAGCACTCAACCTCTGGGTGGA 855  
Db 100 GlyProThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGlyGly 119  
Qy 856 CCATCCGTCTTCATCTCTCCCTCCAAAGATCAAGATGTACTCATGATCTCCCTGAGCCCC 915



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Db      120 ProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerPro 139
QY      916 ATAGTCACATGTGTGGTGGATGTGAGCGAGATGACCCAGATGTCCAGATCAGCTGG 975
Db      140 IleValThrCysValValValAspValSerGluAspProAspValGlnIleSerTrp 159
QY      976 TTGTGAACAACTGGAAGTACACAGCTCAGACACAAACCCATAGAGAGGATTACAAC 1035
Db      160 PheValAsnAsnValGluValHisThrAlaGlnThrHisArgGluAspTyrAsn 179
QY      1036 AGTACTCTCGGGTGTGTCAGTGCCTCCCATCCAGCACCAGACTGGATGAGTGCAG 1095
Db      180 SerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLys 199
QY      1096 GAGTTCAAATGCAAGTCAACAAAGACCTCCAGCGCCATCCAGAGAACCATCTCA 1155
Db      200 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSer 219
QY      1156 AAACCAAGGGTCAGTAAGAGCTCCACAGGTATATGTCTTGCTCCACAGAAAGAG 1215
Db      220 LysProLysGlySerValArgAlaProGlnValTyrValLeuProProGluGluGlu 239
QY      1216 ATGACTAAGAAACAGTCACTGTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1275
Db      240 MetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIle 259
QY      1276 TAGCTGGAGTGGACCAACAGCGGAAACAGAGCTAACTACAGAACACTGAACACAGTC 1335
Db      260 TyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProVal 279
QY      1336 CTGGACTCTGATGTTCTTACTTCACTGTACAGCAAGCTGAGAGTGGAAGAAAGAACTGG 1395
Db      280 LeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrp 299
QY      1396 GTGGAAGAAATAGTACTCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1455
Db      300 ValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisThr 319
QY      1456 ACTAAGAGCTTCTCCCGGACTCCGGGT 1482
Db      320 ThrLysSerPheSerArgThrProGly 328

RESULT 13
ID AAR47450
XX AAR47450 standard; protein; 477 AA.
XX AAR47450;
XX
XX 25-MAR-2003 (revised).
XX 24-JUN-1994 (first entry)
XX
XX T84.12 Heavy chain.
XX
XX Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region;
XX transform; myeloma cell; light chain; tumour.
XX
XX Synthetic.
XX
XX WO9325237-A1.
XX
XX 23-DEC-1993.
XX
XX 15-JUN-1993; 93WO-US005709.
XX
XX 15-JUN-1992; 92US-00904074.
XX
XX (YANG/) YANG Y.
XX (CITY ) CITY OF HOPE.
XX
XX Shively JE, Fischer R, Wu A, Paxton R, Yang YH;
XX WPI; 1994-007204/01.
XX

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DR      N-PSDB; AAQ54652.
XX
XX New chimeric T 84.12 antibody active against carcinoembryonic antigen -
PT has murine variable and human constant regions, also DNA encoding it and
PT transformed myeloma cells.
XX
XX Claim 1; Page 17; 27pp; English.
XX
XX The sequences (AAQ54651-52) show the light and heavy chain CDNA of
CC murine T84.12. The T84.12 antibody is directed against the tumour marker
CC carcinoema embryonic antigen, and is useful for tumour imaging and has
CC immunotherapy. The amino acid sequence given in the specification has
CC been incorrectly identified as a nucleic acid sequence, therefore
CC unacceptable characters have been represented as an 'N'. The amino acid
CC sequence given below has been derived from the cDNA, by the indexer.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 477 AA;

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## Alignment Scores:

```

Pred. No.: 1.29e-101 Length: 477
Score: 1310.50 Matches: 270
Percent Similarity: 68.25% Conservative: 18
Best Local Similarity: 63.98% Mismatches: 39
Query Match: 48.63% Indels: 95
DB: 2 Gaps: 10

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US-10-048-116-1 (1-1484) x AAR47450 (1-477)

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QY      250 CAAGTGGAGCTGCAAAACATAGCTGCAGAAAACAACTTGGGAATCTTGACTAAGAG 309
Db      139 GlnGlyThrLeuAlaThrValSerAlaAlaLys----- 149
QY      310 TCAATTTTCACTCCAGCTACCAATGAGGCTCCTCAAGCGACTGTGTTCCTCCCAAGTCCCT 369
Db      150 -----ThrThrAlaPro-----SerValTyrProLeuAlaPro 160
QY      370 GTG-----CTGCTGGTGCAGCCCAACACCTTATCTGCTTTTGTGACAACTCTTC 420
Db      161 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe 180
QY      421 CCACCTGTGATCAACATCATCATGGCTCAAGATAGCAATAGCACTGATCAGACGGCGTTTAT 480
Db      181 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 197
QY      481 GAGACGAGCTTCTCGTCAACCGTGACCATTCCTTCCCAAGCTGTCTTATCTCACCTTC 540
Db      198 -----HisThrPheProAlaVal----- 203
QY      541 ATCCCTTCTGATGATGATGATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCCG 600
Db      204 -----LeuGlnSerAspLeuTyrThrLeuSer----- 212
QY      601 GTTCTGAAACACTGGGAACCTGAGATTCCAGCCCCCATCTCAGCTGAGCTGACAGAACTGGA 660
Db      213 -----SerSerThr----- 218
QY      661 GGTGGAGGATCCACTACAGCTCCACTCAGCTCAGCTCGAAAGAGAGCTCCAGGCCCTGGAG 720
Db      219 -----SerSerThr----- 221
QY      721 AAGGAAATGCACAGCTGGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGCA 780
Db      222 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 234
QY      781 GCATCT-----GAGCCAGAGGGCCCAACAATCAAGCCCTGT 816
Db      235 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 254
QY      817 CCTCATGCAAAATGCCAGCACCTAACCTTCTTGGGTGGAGCACTCCGCTTCATCTCCCT 876
Db      255 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 274

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Qy 877 CCAAGATCAAGGATGACTCATGATCTCCCTGAGCCCACTAGTACATGATGTTGGTGTG 936  
 Db |||||  
 Qy 275 ProlysisLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeuVal 294  
 Db |||||  
 Qy 937 GATGTGAGCGAGATGATCCAGATGTCAGATCAGCTGGTTTGTGAACAAGCTGGAAGTA 996  
 Db |||||  
 Qy 295 AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal 314  
 Db |||||  
 Qy 997 CACACAGCTCAGACACAAACCATAGAGAGATTACACAGTACTCTCCGGTGGTCACT 1056  
 Db |||||  
 Qy 315 HisThrAlaGlnThrGlnThrHisArgGluAspTrpAsnSerThrLeuArgValValSer 334  
 Db |||||  
 Qy 1057 GCGCTCCCATCCAGCACAGGACTGGATGATGGCAAGGAGTTCAAATGCAAGCTCAAC 1116  
 Db |||||  
 Qy 335 AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn 354  
 Db |||||  
 Qy 1117 AACAAAGACCTCCAGCGCCCATCGAGAGAACCAATCTCAAACCCAAAGGTCAGTAAGA 1176  
 Db |||||  
 Qy 355 AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg 374  
 Db |||||  
 Qy 1177 GCTCCACAGGTATATGCTTGCCTCCACCAGAACAGATGACTAAGAAACAGGTCACT 1236  
 Db |||||  
 Qy 375 AlaProGlnValTyValLeuProProProGluGluMetThrLysLysGlnValThr 394  
 Db |||||  
 Qy 1237 CTGACCTGCATGTCACAGACTTTCATGCTGAAGACATTTACGTGGAGTGGACCAAC 1296  
 Db |||||  
 Qy 395 LeuThrCysMetValThrAspPheMetProGluAspIleTyValGluTrpThrAsnAsn 414  
 Db |||||  
 Qy 1297 GGGAAAACAGAGCTAACTACAAGAACACTGAACACAGTCTCTGGACTCTGATGGTCTTAC 1356  
 Db |||||  
 Qy 415 GlyLysThrGluLeuAsnTyLysAsnThrGluProValLeuAspSerAspGlySerTy 434  
 Db |||||  
 Qy 1357 TTCATGTACACAGCTGAGGTGGAAAGAGAACTGGGTGGAAAGAAATAGTACTCTC 1416  
 Db |||||  
 Qy 435 PheMetTySerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTySer 454  
 Db |||||  
 Qy 1417 TGTTCAGTGGTCCACGAGGGTCTGCACAAATCACACAGCTAAGAGCTTCTCCCGGACT 1476  
 Db |||||  
 Qy 455 CysSerValValHisGluGlyLeuHisAsnTyHisThrLysSerPheSerArgThr 474  
 Db |||||  
 Qy 1477 CCGGGT 1482  
 Db |||||  
 Qy 475 ProGly 476  
 Db |||||  
 RESULT 14  
 ID ADL15169 standard; protein; 329 AA.  
 XX AC ADL15169;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Murine immunoglobulin G2a (IgG2a) protein.  
 XX KW Modified s immunoglobulin antibody; constant region; immunoglobulin; Ig;  
 KW IgG2a; modified s antibody; S-Ab; immune disorder; infectious disorder;  
 KW cancerous disorder; murine; antineumatic; antiarthritic; osteopathic;  
 KW antiinflammatory; dermatological; immunosuppressive; ophthalmological;  
 KW antibacterial; virucide; anti-HIV; vasotropic; antiallergic;  
 KW hepatotropic.  
 XX OS Mus sp.  
 XX PN US2003232046-A1.  
 XX XX  
 XX PD 18-DEC-2003.  
 XX PF 05-JUN-2003; 2003US-00454948.  
 XX XX  
 XX PR 14-JUN-2002; 2002US-0388896P.  
 XX (SCAL/) SCALLON B J.  
 XX PA (CAIA/) CAI A.  
 XX PA

(NASO/) NASO M.  
 Scallon BJ, Cai A, Naso M;  
 WPI; 2004-052145/05.  
 Modified s immunoglobulin molecule useful for treating immune disorder or diseases especially immune conditions e.g. rheumatoid arthritis, osteoarthritis, inflammatory bowel disease or systematic lupus erythematosus.  
 Example 1; SEQ ID NO 1; 37pp; English.  
 The present invention relates to modified "S" immunoglobulin antibodies that have an extra constant region immunoglobulin (Ig) domain inserted into the constant region of the Ig molecule. Preferably, the extra constant region Ig domain comprises a CH3, CH1 or CH2 domain, and the Ig molecule is IgG1, where the extra constant region Ig domain comprises a CH1 domain of an IgG2a immunoglobulin. The modified "s" antibody (S-Ab) is useful for treating immune disorders (e.g. rheumatoid arthritis/seronegative arthropathies, osteoarthritis, inflammatory bowel disease, systematic lupus erythematosus, iridocyclitis/uveitis/optic neuritis, idiopathic pulmonary fibrosis, systemic vasculitis/wegener's granulomatosis), and infectious or cancerous disorders (e.g. chronic bacterial infection, acute and chronic parasitic or infectious processes, including bacterial, viral and fungal infections, HIV infection/HIV neuropathy, meningitis, hepatitis, septic arthritis, peritonitis, pneumonia, epiglottitis). The present sequence represents murine IgG2a protein.  
 SQ Sequence 329 AA;  
 Alignment Scores:  
 Pred. No.: 2.48e-101 Length: 329  
 Score: 1306.50 Matches: 263  
 Percent Similarity: 71.47% Conservative: 15  
 Best Local Similarity: 67.61% Mismatches: 34  
 Query Match: 48.48% Indels: 77  
 DB: 8 Gaps: 8  
 US-10-048-116-1 (1-1484) x ADL15169 (1-329)  
 Qy 349 ACTGTGTTCCCAAGTCCCTCTGTG-----CTGCTGGGTGAGCCCAACACCCCTTATC 399  
 Db |||||  
 Db 6 SerValTyProLeuAlaProValCysGlyAspThrThrGlySerSerValThrLeuGly 25  
 Qy 400 TGCTTTGTGGACAACTCTTCCACCTGTGATCAATCATCATGGCTCAGAAATAGCAAG 459  
 Db |||||  
 Db 26 CysLeuValLysGlyTyPheProGluProValThrLeuThrTrp-----AsnSerGly 43  
 Qy 460 TCAGTCACAGCGCGTTTATGAGACCAGTCTCTCTCAACCGTGACCATTCCTTCCAC 519  
 Db |||||  
 Db 44 SerLeuSerSerGlyVal-----HisThrPhePro 53  
 Qy 520 AAGCTGTCTTATCTCACCTTTCATCTCTGATGATGATGATGATGATGATGATGATGATG 579  
 Db |||||  
 Db 54 Alaval-----LeuGlnSerAspLeuTyThrLeuSer----- 64  
 Qy 580 CACTGGGGCCTGGAGGAGCGGTTCTGAAACACTGGGAACCTGAGATTCACAGCCCCCATG 639  
 Db |||||  
 Db 64 ----- 64  
 Qy 640 TCAGAGCTGACAGAACTGGAGGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAA 699  
 Db |||||  
 Db 65 SerSerValThrValThr-----SerSerThr----- 73  
 Qy 700 AAAGAGCTCCAGGCCCTGGAGAGGAAATGCACAGCTGGAATGGAGTTTGCAGACTG 759  
 Db |||||  
 Db 74 -----TrpProSerGlnSerIle 79  
 Qy 760 GAAAAGGAACCTGGCTCAGGAGCATCTGAG-----CCGAGA 795  
 Db |||||  
 Db 80 ThrCysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleAlaProArg 99

```
QY 796 GGGCCCAACAATCAAGCCCTGTCTCCATGCAAAATGCCAGACCTAACCTTTGGGTGA 855
Db 100 GlyProThrIleLysProCysProCysLysCysProAlaProAsnLeuLeuGlyGly 119
QY 856 CATCCGCTTCTCATCTCCCTCAAAAGATCAAGGATGTAATCATGATCTCCCTGAGCCCC 915
Db 120 ProSerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerPro 139
QY 916 ATAGTCACATGTCTGTGTGGATGAGCGAGGATGCCAGATGCCAGATCTCCAGATCAGCTGG 975
Db 140 IleValThrCysValValValAspValSerGluAspProAspValGlnIleSerTrp 159
QY 976 TTTGTGAACAACGCTGAAGTACACACAGCTCAGACACAAACCATAGAGAGATTACAAAC 1035
Db 160 PheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTrpAsn 179
QY 1036 AGTACTCTCCGGGTGTGATGCTCCCTCCCATCCAGCACAGACTGGATGATGGCAAG 1095
Db 180 SerThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLys 199
QY 1096 GAGTTCAATGCAAGTCAACAAAGACCTCCAGCGCCCATCGAGAGAACCACTCTCA 1155
Db 200 GluPheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSer 219
QY 1156 AAACCCAAAGGCTCAGTAAGAGCTCCACAGGTATATGTCTGCTCCACAGAGAAGAG 1215
Db 220 LysProLysGlySerValArgAlaProGlnValTrpValLeuProProGluGlu 239
QY 1216 ATGACTAAGAAACAGGTCACTCTGACCTGATGGTCACAGATTCATGCTGAAGACATT 1275
Db 240 MetThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIle 259
QY 1276 TAGCTGGAGTGCACCAACACCGGAAACAGAGCTAACTACAGAACACTGAACAGTC 1335
Db 260 TyrValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTrpLysAsnThrGluProVal 279
QY 1336 CTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAGCTGAGAGTGGAAGAACTGG 1395
Db 280 LeuAspSerAspGlySerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrp 299
QY 1396 GTGGAAGAAATAGTACTCTGTTTCAGTGGTCCAGCGGTCTGCACAAATCACACAG 1455
Db 300 ValGluArgAsnSerTyrSerCysSerValValHisGluGlyLeuHisAsnHisThr 319
QY 1456 ACTAAGAGCTTCTCCGGACTCCGGGT 1482
Db 320 ThrLysSerPheSerArgThrProGly 328

RESULT 15
AAP93037
ID AAP93037 standard; protein; 447 AA.
XX
AC AAP93037;
XX
DT 25-MAR-2003 (revised)
DT 14-MAR-1990 (first entry)
XX
DE Chimeric antibody heavy chain variable region.
XX
KW KS1/4; chimeric antibody; heavy chain variable region.
XX
OS Mus.
XX
PN BP38767-A..
XX
PD 25-OCT-1989..
XX
PF 18-APR-1989; 89EP-00303814..
XX
PR 21-APR-1988; 88US-00184522..
XX
PA (ELIL ) LILLY & CO ELI.
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XX Beavers LS, Bumol T, Galski RA, Weigel BJ;
PI WPI: 1989-311203/43.
DR N-PSDB; AAN91659.
XX Recombinant DNA cpds. producing antibodies - monoclonal and chimeric
PT derived from monoclonal antibody KS1/4.
XX Claim 6; Page 50; 89pp; English.
XX The sequence encodes the heavy chain of Mab KS1/4, used to construct
CC mouse/human chimeric antibodies. KS1/4 is a murine antibody which binds
CC to surface antigens on adenocarcinoma cells and the use of human C
CC regions avoids immunological problems during treatment. (Updated on 25-
CC MAR-2003 to correct PD field.) (Updated on 25-MAR-2003 to correct PA
CC field.) (Updated on 25-MAR-2003 to correct FI field.)
XX
SQ Sequence 447 AA;
Alignment Scores:
Pred. No.: 3 33e-101 Length: 447
Score: 1305.50 Matches: 264
Percent Similarity: 70.65% Conservative: 20
Best Local Similarity: 65.67% Mismatches: 41
Query Match: 48.44% Indels: 77
DB: 1 Gaps: 8
US-10-048-116-1 (1-1484) x AAP93037 (1-447)
QY 310 TCAAATTTTCAACCCAGCTACCAATGAGGCTCTCAAGCGACTGTGTCCCAAGTCCCT 369
Db 111 ThrSerValThrValSerSerAlaLysThrThrAlaProSerValTrpProLeuAlaPro 130
QY 370 GTG-----CTGCTGGTCTAGCCCAACACCTTATCTGCTTGTGTGACAACTCTTC 420
Db 131 ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTrpPhe 150
QY 421 CCACCTGTGATCAACATCACATGCTGCTCAGAAATAGCAAGTCAGTCACAGACGGCTTAT 480
Db 151 ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal--- 167
QY 481 GAGACAGCTTCTCTGTCACACGTCAGCACTTCTTCCCAAGCTGTCTTATCTCACCTTC 540
Db 168 -----HisThrPheProAlaVal----- 173
QY 541 ATCCCTTCTGATGATGACATTTATGACTGCAAGTGGAGCACTGGGGCTCGAGGAGCCG 600
Db 174 -----LeuGlnSerAspLeuTyrThrLeuSer----- 182
QY 601 GTTCTGAAACACTGGGACCTGAGATTCAGCCCCCATGTCTAGAGCTGACAGAACTGGA 660
Db 183 -----SerSerValThrValThr----- 188
QY 661 GGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAATAAGAGCTCCAGGCTCGAG 720
Db 189 -----SerSerThr----- 191
QY 721 AAGGAAATGACACAGCTGGAATGGAGTTGGAAGCACTGGAAGAACTGCTCAGGCA 780
Db 192 -----TrpProSerGlnSerIleThrCysAsnValAlaHisPro 204
QY 781 GCATCT-----GAGCCCAAGGGCCCAACATCAAGCCCTGT 816
Db 205 AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys 224
QY 817 CCTCATGCAAAATGCCAGCACCTAACTCTTGGGTGGACCACTCCGCTTCTTCTTCCCT 876
Db 225 ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro 244
QY 877 CCAAGATCAAGATGTACTCATGATCTCCCTGAGCCCCCATGTCATGTGTGTGGTG 936
Db 245 ProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValVal 264
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Qy	937	GATCTGACGAGGATGACCCAGATGTCAGATCAGCTGGTTTGTGAACAACGTCGAAGTA	996
Db	265	AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal	284
Qy	997	CACACAGCTCAGACACAAACCATAGAGAGGATTACAACTACTCTCCGGGTGGTCAGT	1056
Db	285	HisThrAlaGlnThrGlnThrHisArgGluAspIlyrAsnSerThrLeuArgValValSer	304
Qy	1057	GCCCTCCCCATCCAGCACACAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC	1116
Db	305	AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn	324
Qy	1117	AACAAAGACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTAAGA	1176
Db	325	AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg	344
Qy	1177	GCTCCACAGGTATATGCTTTCCTCCACAGAGAGAGATGACTAAGAAACAGGTCACCT	1236
Db	345	AlaProGlnValTyrValLeuProProProGluGluMetThrLysLysGlnValThr	364
Qy	1237	CTGACCTGCATGGTCACAGACTTCATCCCTGAAGACATTTACGTGGAGTGGACCAACAAC	1296
Db	365	LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsn	384
Qy	1297	GGGAAACAGAGCTAAACTACAGAACACTGAACAGTCCCTGGACTCTGATGGTTCTTAC	1356
Db	385	GlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr	404
Qy	1357	TTCATGTACAGCAAGCTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAGAAATAGCTACTCC	1416
Db	405	PheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSer	424
Qy	1417	TGTTTCAGTGGTCCAGAGGGTCTGCACAATCACACACGACTAAGAGCTTCTCCCGGACT	1476
Db	425	CysSerValValGlnGluGlyLeuHisAsnHisThrThrLysSerPheSerArgThr	444
Qy	1477	CCGGGT 1482	
Db	445	ProGly 446	

Search completed: June 16, 2005, 02:41:41  
Job time : 254.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 16, 2005, 01:36:27 ; Search time 276.5 Seconds

(without alignments)  
5496.749 Million cell updates/sec

Title: US-10-048-116-1

Perfect score: 2695

Sequence: 1 atgcgcgtcagcagagctct.....ttctcccgactccgggtaa 1484

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p,model -DEV=xlp  
-Q/cgn2.1/USFTO\_spool\_p/US10048116/runat\_15062005\_125142\_29750/app\_query.fasta\_1.1671  
-DB=UniProt -Qfmt=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdd -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10048116@CGN 1.1 307 @runat\_15062005\_125142\_29750 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: uniprot\_sprot.\*
- 2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1313.5	48.7	330	1 GCAA_MOUSE	P01863 mus musculus
2	1313.5	48.7	339	1 GCAM_MOUSE	P01865 mus musculus
3	1297	48.1	472	2 Q6PUA7	Q6pja7 mus musculus
4	1294.5	48.0	471	2 Q66K04	Q66k04 mus musculus
5	1291.5	47.9	464	2 Q6PF95	Q6pf95 mus musculus
6	1291.5	47.9	464	2 Q6PIP8	Q6pip8 mus musculus
7	1291.5	47.9	465	2 Q6PJB2	Q6pjb2 mus musculus
8	1182	43.9	256	1 HA2D_MOUSE	F04228 mus musculus
9	1161	43.1	256	2 Q6SR48	Q6sr48 mus musculus
10	1107	41.1	256	2 Q8K2X0	Q8k2x0 mus musculus
11	1100	40.8	256	2 Q860C1	Q860c1 mus musculus
12	1078	40.0	256	1 HA2B_MOUSE	E14434 mus musculus
13	1075	39.9	256	1 HA2K_MOUSE	P01910 mus musculus
14	1058.5	39.3	473	2 Q9D8I4	Q9d8i4 mus musculus
15	1057	39.2	254	1 HA2J_MOUSE	P23150 mus musculus
16	1048	38.9	254	2 Q9TQ71	Q9tg71 mus musculus

17	1048	38.9	254	2	Q9TQ72	Q9tg72 mus musculus
18	1037	38.5	335	1	GCAB_MOUSE	P01864 mus musculus
19	1018.5	37.8	473	2	Q91Z05	Q91z05 mus musculus
20	1017.5	37.8	474	2	Q8R3H6	Q8r3h6 mus musculus
21	1012.5	37.6	336	1	GCB_MOUSE	P01866 mus musculus
22	1012.5	37.6	405	1	GBW_MOUSE	P01867 mus musculus
23	1005	37.3	233	1	HA2F_MOUSE	P14435 mus musculus
24	1000	37.1	233	1	HA2R_MOUSE	P14436 mus musculus
25	996	37.0	233	1	HA2S_MOUSE	P14437 mus musculus
26	972	36.1	256	1	HA2B_RAT	P20037 rattus norv
27	964	35.8	256	2	O8VI32	O8vi32 rattus norv
28	951	35.3	252	2	Q7ORH9	Q7orh9 rattus norv
29	939	34.8	227	1	HA2U_MOUSE	P14438 mus musculus
30	937.5	34.8	255	2	Q6MGA0	Q6mga0 rattus norv
31	929	34.5	221	1	HA2Q_MOUSE	P04227 mus musculus
32	929	34.5	256	2	Q95572	Q95572 rattus norv
33	929	34.5	333	1	GCB_RAT	P20761 rattus norv
34	929	34.5	470	2	Q7THK1	Q7thk1 mus musculus
35	927.5	34.4	256	2	Q8HWL3	Q8hw13 sigmodon hi
36	923.5	34.3	329	1	GC3_MOUSE	P22436 mus musculus
37	917.5	34.0	398	1	GC3M_MOUSE	P03987 mus musculus
38	881.5	32.7	458	2	Q65ZQ1	Q65zq1 homo sapien
39	880.5	32.7	463	2	Q99LC4	Q99lc4 mus musculus
40	880	32.7	329	1	GCC_RAT	P20762 rattus norv
41	876	32.5	478	2	Q6FI81	Q6fi81 homo sapien
42	873.5	32.4	475	2	Q6N095	Q6n095 homo sapien
43	872	32.4	227	2	Q31247	Q31247 peromyscus
44	872	32.4	470	2	Q6BJA4	Q6bj44 homo sapien
45	870	32.3	475	2	Q6MZQ6	Q6mzq6 homo sapien

ALIGNMENTS

RESULT 1

GCAA\_MOUSE STANDARD; PRT; 330 AA.  
AC P01863;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE I9 gamma-2A chain C region, A allele.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81076554; PubMed=6777755;  
RA Sikorav J.-L., Auffray C., Rougeon F.;  
RT "Structure of the constant and 3' untranslated regions of the murine  
RT Balb/c gamma 2a heavy chain messenger RNA.";  
RL Nucleic Acids Res. 8:3143-3155(1980).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81198976; PubMed=6262729;  
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;  
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene  
RT and evolution of heavy chain genes; further evidence for intervening  
RT sequence-mediated domain transfer.";  
RL Nucleic Acids Res. 9:1365-1381(1981).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81223894; PubMed=6787604;  
RA Ollo R., Auffray C., Mochamps C., Rougeon F.;  
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes  
RT suggests that exons can be exchanged between genes in a multigenic  
RT family.";  
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).  
RN [4]  
RP MYELOMA PROTEIN MOPC 173.  
RX MEDLINE=74175517; PubMed=4831970;  
RA Bourgois A., Fougereau M., Rocca-Serra J.;  
RT "Determination of the primary structure of a mouse IgG2a

immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";  
 Eur. J. Biochem. 43:423-435(1974).  
 [5]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=7305687; PubMed=4565406;  
 RA de Preval C., Fougereau M.;  
 RT "Determination of the primary structure of a mouse gamma G2a  
 RI immunoglobulin. Identification of the disulfide bridges.";  
 RL Eur. J. Biochem. 30:452-462(1972).  
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

EMBL; V00798; CAA24178.1; -;  
 PIR; A02152; G2MSA.

PDB; 1E4W; X-ray; H=1-99.  
 PDB; 1E4X; X-ray; H/I=1-103.  
 PDB; 1MNU; X-ray; H=1-103.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00407; IGL1; 2.  
 DR PROSITE; PS0835; IG\_LIKE; 3.  
 DR PROSITE; PS0290; IG\_MHC; 1.  
 KW 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.

FT NON\_TER 1 1  
 FT DOMAIN 6 98 Ig-like 1.  
 FT DOMAIN 121 220 Ig-like 2.  
 FT DOMAIN 229 325 Ig-like 3.  
 FT DISULFID 15 15 Interchain (with a light chain).

FT DISULFID 27 82  
 FT DISULFID 107 107 Interchain (with a heavy chain).  
 FT DISULFID 110 110 Interchain (with a heavy chain).  
 FT DISULFID 112 112 Interchain (with a heavy chain).  
 FT DISULFID 144 204  
 FT DISULFID 250 308

FT STRAND 4 4  
 FT STRAND 7 11  
 FT STRAND 22 33  
 FT STRAND 38 41  
 FT STRAND 42 44  
 FT TURN 45 45  
 FT TURN 46 46  
 FT STRAND 50 52  
 FT STRAND 56 56  
 FT TURN 59 60  
 FT TURN 62 71  
 FT TURN 72 77  
 FT STRAND 81 86  
 FT HELIX 87 89  
 FT TURN 90 90  
 FT STRAND 91 96  
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

## Alignment Scores:

Pred. No.: 1,21e-87 Length: 330  
 Score: 1313.50 Matches: 267  
 Percent Similarity: 71.03% Conservative: 15  
 Best Local Similarity: 67.25% Mismatches: 36  
 Query Match: 48.74% Indels: 79  
 DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x GCAA\_MOUSE (1-330)

QY 325 GCTACCAATGAGGCTCCTCAAGCGACTGTGTGCCCAAGTCCCTGTG-----CTG 375

Db 1 AlalysThrThrAlaPro-----SerValTyrProLeuAlaProValCysGlyAspThr 18  
 QY 376 CTGGTCAGGCCCAACACCCCTTATCTGCTTTGTGGCAACAACATCTTCCACCTGTGATCAAC 435  
 Db 19 ThrGlySerSerValThrLeuGlyCysLeuValGlyTyrPheProGluProValThr 38  
 QY 436 ATCATGCTGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACAGCTTCTCTC 495  
 Db 39 LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal----- 50  
 QY 496 GTCAACCGTGACCATCTCTTCCACAAGCTGCTTATCTCACCTTCTCATCTTCTGTGATGAT 555  
 Db 51 -----HisThrPheProAlaVal-----LeuGlnSer 59  
 QY 556 GACATTTTATGACTGCACAGGTGGAGCACTGGGGCTTGAGGAGCGGGTCTTGTAAACACTGG 615  
 Db 60 AspleuTyrThrLeuSer----- 65  
 QY 616 GAACCTGAGATTCCAGCCCCCATGTCTAGAGCTGACAGAAACTGGAGGTGGAGGATCCACT 675  
 Db 66 -----SerSerValThrValThr-----SerSer 73  
 QY 676 ACAGCTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGAGAAATGACAG 735  
 Db 74 Thr----- 74  
 QY 736 CTGGAATGGAGTTGCAAGCACTGAAAAAGAACTGGCTCAGGAGCATCT----- 786  
 Db 75 -----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLys 92  
 QY 787 -----GAGCCCAAGAGGGCCCAACATCAAGCCCTGTCTCTCATGCAAAATGC 831  
 Db 93 ValAspLysLysIleGluProArgGlyProThrIleLysProCysProCysLysCys 112  
 QY 832 CCAGCACTTAACCTCTTTGGGTGACCACTCGTCTTCTATCTTCCCTCCAAAGATCAAGAT 891  
 Db 113 ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 132  
 QY 892 GTACTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGTGGTGGTGGTGGTGGTGG 951  
 Db 133 ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp 152  
 QY 952 GACCCAGATGTCAGATCAGCTGGTTGTGAACACGTCGAAGTACACAGCTCAGCTCAGACA 1011  
 Db 153 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 172  
 QY 1012 CAAACCCATAGAGAGGATTACAAACAGTACTCTCGGGTGGTGGTGGTGGTGGTGGTGGTGG 1071  
 Db 173 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 192  
 QY 1072 CACCAGACTGGATGATGGCAAGGAGTTCAAAATGCAAGGTCAACAAACAAAGACCTCCCA 1131  
 Db 193 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro 212  
 QY 1132 GCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCACTAAGAGTCCACAGGTATAT 1191  
 Db 213 AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr 232  
 QY 1192 GTCTTGCTCCACACAGAGAGAGATGACTAAGAAACAGGTCTACTCTGACCTGCTGCTGCTC 1251  
 Db 233 ValLeuProProGluGluGluMetThrLysLysGlnValThrLeuThrCysMetVal 252  
 QY 1252 ACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAACCGGAAACAGAGCTA 1311  
 Db 253 ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu 272  
 QY 1312 AACTAGAGAACACTGAACCACTGCTGGACTCTGATGGTTCTTACTTCTCATGTGACAGCAAG 1371  
 Db 273 AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys 292  
 QY 1372 CTGAGAGTGGAAAAGAGAACTGGGTGGAAGAAATAGCTACTCTCTCTGCTGCTGCTGCTGCT 1431

```
Db 293 LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis 312
QY 1432 GAGGGTCTGCACAAATACACACAGACTAAGAGGCTTCTCCCGGACTCCGGGT 1482
Db 313 GluGlyLeuHisAsnHisThrThrLysSerPheSerArgThrProGly 329
RESULT 2
GCAM_MOUSE
ID GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01865;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig gamma-2A chain C region, membrane-bound form.
GN Name-IgH-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=Displayed;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=External;
CC Note=Probably the major isoform;
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00471; AAB59661.1; ALT_INIT.
DR PIR: A02154; G2MSAM.
DR PDB: 1KB5; X-ray; H=1-100.
DR PDB: 1ORQ; X-ray; B=1-101.
DR PDB: 1YES; X-ray; H=1-99.
DR MGD: MGI:96443; IgH-1a.
DR GO: GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO: GO:0003823; P:antigen binding; IDA.
DR GO: GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO: GO:0006958; P:complement activation, classical pathway; IDA.
DR GO: GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO: GO:0050728; P:negative regulation of inflammatory response; IDA.
DR GO: GO:0006910; P:phagocytosis, binding; IDA.
DR GO: GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO: GO:0050778; P:positive regulation of immune response; IDA.
DR GO: GO:0050729; P:positive regulation of inflammatory response; IDA.
DR GO: GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO: GO:0016068; P:type I hypersensitivity; IDA.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 2.
DR SMART: SM00407; IGc1; 2.
DR PROSITE: PS00835; IG LIKE; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW 3D-structure; Alternative splicing; Glycoprotein;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat; Transmembrane.
FT NON_TER 1
FT DOMAIN 6 98 Ig-like 1.
FT DOMAIN 121 220 Ig-like 2.
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FT DOMAIN 229 325
FT DISULFID 15 15
FT DISULFID 27 82
FT DISULFID 107 107
FT DISULFID 110 110
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT CARBOHYD 180 180
FT STRAND 4 4
FT STRAND 7 11
FT STRAND 22 33
FT STRAND 38 41
FT STRAND 42 44
FT TURN 45 45
FT STRAND 46 46
FT TURN 48 49
FT STRAND 50 58
FT TURN 59 60
FT STRAND 61 71
FT TURN 72 77
FT STRAND 81 86
FT HELIX 87 89
FT TURN 90 90
FT STRAND 91 96
SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;

Alignment Scores:
Pred. No.: 1.26e-87 Length: 399
Score: 1313.50 Matches: 267
Percent Similarity: 71.03% Conservative: 15
Best Local Similarity: 67.25% Mismatches: 36
Query Match: 48.74% Indels: 79
DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x GCAM_MOUSE (1-399)
QY 325 GTTACCAATGAGGCTCTCAAGCGACTGTTTCCCAAGTCCCTGTG-----CTG 375
Db 1 AlaLysThrAlaPro-----SerValTyrProLeuAlaProValCysGlyAspThr 18
QY 376 CTGGGTGAGCCCAACACACCTTATCTGCTTGTGGCAACATCTTCCACCTGTGATCAAC 435
Db 19 ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr 38
QY 436 ATCAGATGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACAGCTTCCTC 495
Db 39 LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal-----50
QY 496 GTCAACCGTGACATCTCTCCACAGCTGTCTTATCTCACCTTCATCTCTCTGTGATGAT 555
Db 51 -----HisThrPheProAlaVal-----LeuGlnSer 59
QY 556 GACATTTATGACTGCAAGGTGGAGCACTGGGGCTGGAGAGCGGTTCTGAAACACTGG 615
Db 60 AspLeuTyrThrLeuSer-----65
QY 616 GAACCTGAGATTCCAGCCCCCCTTCAGAGCTGACAGAACTGGAGGTGGAGGATCCACT 675
Db 66 -----SerSerValThrValThr-----SerSer 73
QY 676 ACAGTCCATCAGCTCAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAGAAATGCACAG 735
Db 74 Thr-----74
QY 736 CTGGAATGGAGTTGCAAGCACTGGAAGAAAGAACTGGCTCAGGACGACATCT-----786
Db 75 -----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerSerThrLys 92
QY 787 -----GAGCCCGAGAGGGCCCAACATCAAGCCCTGTCTCCATGCAATATGC 831
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QY 167 -----ATGAGTTGT----- 175
Db SerGlyAlaGluLeuValArgProGlyAlaSerValLysLeuSerCysLysAlaSerGly 45
QY 176 -----TCTATGGGACT-----TGGATAAGAAGAAACTGCTGGAGGCTT----- 216
Db TyrIlePheThrSerTyrTrpIleHisTrpValLysGlnArgSerGlyGlnGlyLeuGlu 65
QY 217 -----CTGAGTTGGCCAAATTGATATCTTTTTCAGCCCAAGGTGGA 258
Db TrpIleAlaArgIleTyrProGlyThrGlySerThrTyrTrpAsnGluLysPheLysGly 85
QY 259 CTGCAAAACATAGCTCAGAAAAACAACTTGGGAATCTTGACTAAGAGGTCAAATTTTC 318
Db LysAlaThrLeuThrAlaAspLysSerSerThrAlaPheMetGlnLeuSerSerLeu 105
QY 318 ----- 318
Db LysSerGluAspSerAlaValTyrPheCysAlaTyrGlyTyrAspAlaLeuTyrTrpGly 125
QY 319 -----ACCCAGCTACCAATGAGGCTCTCAAGCGACT-----GTGTTCCCAAG 363
Db GlnGlyThrProIleThrValSerSerAlaLysThrAlaProSerValTyrProLeu 145
QY 364 TCCCTGTG-----CTGCTGGGTGAGCCCAACACCTTATCTGCTTTTGTGGACAAC 414
Db AlaProValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGly 165
QY 415 ATCTTCCCACTGTGATCAACATCAGATGGCTCAGAAATAGCAAGTCAGTCACAGACGGC 474
Db TyrPheProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGly 183
QY 475 GTTTATGAGACCACTCTCTCGTCAACCGTGACCATTCCTTCCACAGCTGTCTTATCTC 534
Db Val-----HisThrPhePro----- 188
QY 535 ACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGAGCAGCTGGGGCTGGAG 594
Db -----ValValLeuGlnSerAspLeuTyrThrLeuSer----- 199
QY 595 GAGCCGGTCTGAAACACTGGGAACCTGAGATTCAGCCGCCCATGTCAGAGCTGACAGAA 654
Db -----SerSerValThrVal 204
QY 655 ACTGAGGTGAGGATCCACTACAGCTCCATCAGCTCAGCTCAGTCCGAAAAGAGCTCCAGGCC 714
Db Thr-----SerSerThr----- 208
QY 715 CTGGAAGAAGGAAATGCACAGCTGGAATGGAGTTCGAAGCACTGGAAAAGGAACCTGGCT 774
Db -----TrpProSerGlnSerIleThrCysAsnValAla 219
QY 775 CAGGCAGCATCT-----GAGCCAGAGGGCCCAACAATCAAG 810
Db HisProAlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLys 239
QY 811 CCTGTCTCTCCATGCAAAATGCCAGCACTTAACCTTGGGTGGACCATCCGCTCTCATC 870
Db ProCysProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIle 259
QY 871 TTCCTCTCCAAAGATCAAGGATGACTCATGATCTCTCTGAGCCCACTAGTCACATGTGTG 930
Db PheProProLysIleLysAspValLeuMetIleSerLeuSerProMetValThrCysVal 279
QY 931 GTGGTGGATGTGACGAGGATGACCCAGATGTCACAGATCAGCTGGTTTGTGAACAACGTC 990
Db ValValAspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnVal 299
QY 991 GAAGTACACACACTCAGACACAAACCCATAGAGAGATTACAAAGTACTCTCCGGGTG 1050
Db GluValLeuThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgVal 319

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QY 1051 GTCAGTGCCTCCCTCCCATCCAGCACAGGACTGGATGAGTGGCAAGAGTTCAAATGCAAG 1110
Db ValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLys 339
QY 1111 GTCACACAAAGAGACTCCAGCGCCATCGAGAGAACCATCTCAAAACCCCAAGGCTCA 1170
Db ValAsnAsnLysAlaLeuProAlaProIleGluArgThrIleSerLysProLysGlySer 359
QY 1171 GTAAGAGCTCCACAGGTATATGCTTGTCCCTCCACACAGAAAGAGAGATGACTAAGAAACAG 1230
Db ValArgAlaProGlnValTyrValLeuProProGluGluGluMetThrLysLysGln 379
QY 1231 GTCACCTCTGACCTGATGTCACAGACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1290
Db ValThrLeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTyrThr 399
QY 1291 AACACGGGAAACAGAGCTAACTACAGAACACACTGACACCACTGCTGCTGCTGCTGCTGCTG 1350
Db AsnAsnGlyLysThrGluLeuAsnTyrLysAsnThrGluProValLeuAspSerAspGly 419
QY 1351 TCTTACTTCTCATGTACAGCAAGCTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAAGAAATAGC 1410
Db SerTyrPheMetTyrSerLysLeuArgValGluLysLysAsnTrpValGluArgAsnSer 439
QY 1411 TACTCTGTGTAGTGTCTCCAGAGGTCTGCAACATCACAACAGCTGCTGCTGCTGCTGCTGCT 1470
Db TyrSerCysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerLeuSer 459
QY 1471 CCGACTCCGGGT 1482
Db 460 ArgThrProGly 463

RESULT 6
QY 6P8P8 PRELIMINARY; PRT; 464 AA.
AC 6P8P8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
OS Hypothetical protein.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M., Uslan T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

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US-10-048-116-1 (1-1484) x Q6SR48 (1-256)

QY 1 ATGCGGTGACGAGAGCTGATTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTC 60  
 DB 1 MetProCysSerArgAlaLeuLeuLeuGlyValLeuAlaLeuAnThrMetLeuSerLeu 20  
 QY 61 TGGGAGGTGAAGACGACATTGAGGCGCCAGCCAGCTAGGCTTCTATGGTACAACTGTTTAT 120  
 DB 21 CysGlyGlyGluAspValIleGluAlaAspHisValGlyPheTyrGlyThrThrValTyr 40  
 QY 121 CAGTCTCTGAGACATGCGCCAGTACACATGAATTTGATGGTGTGATGTTGTTCTAT 180  
 DB 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluLeuPheTyr 60  
 QY 181 GTGGACTTGTGATAAGAAAGAACTGCTGGAGGCTTCTCAGTGTGGCCAAATGATGACTC 240  
 DB 61 ValAspLeuAspIlySylThrValTyrPargLeuProGluPheGlyGlnLeuLeuLeu 80  
 QY 241 TTGTAGCCCCAAGTGGACTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300  
 DB 81 PheGluProGlnGlyGlyLeuGlnAenIleAlaGluLysHisAenLeuGlyIleLeu 100  
 QY 301 ACTAAGAGTCAATTTCCACCCAGCTACCAATGAGCTCTCTCAAGGACTGTGTTCCCC 360  
 DB 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120  
 QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGACAACTCTTC 420  
 DB 121 LysSerProValLeuLeuGlyGlnProHisThrLeuIleCysPheValAspAenIlePhe 140  
 QY 421 CCACCTGTGTATCAACATCATAGCTGGCTCAGAAATAGCAAGTCAGTCACAGCGCGTTTAT 480  
 DB 141 ProProValIleAenIleThrTyrLeuArgAsnSerLysSerValThrAspGlyValTyr 160  
 QY 481 GAGACAGCTTCTGCTCAACCTGACCATCTCTTCCACAAAGCTGTCTTATCTCACCTTC 540  
 DB 161 GluThrSerPheLeuValAlaAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180  
 QY 541 ATCCCTTCTCATGATGACATTTATGACTGCAAGGTGGAGCACTGGGCGCTGGAGGAGCG 600  
 DB 181 IleProSerAspAspIleTyrAspCysLysValGluHisTyrGlyLeuGluGluPro 200  
 QY 601 GTTCTGAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGCAGAGAACT 657  
 DB 201 ValIleuLysHisTyrGluProGluLeuProAlaProMetSerGlyLeuThrGluThr 219

RESULT 10  
 ID Q8K2X0 PRELIMINARY; PRT; 256 AA.  
 AC Q8K2X0;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE H2-Aa protein.  
 GN Name=H2-Aa;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.B.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC029620; AAH29620.1; -;  
 DR HSSP; P14438; IK2D.  
 DR MGD; MGI:95895; H2-Aa.  
 DR GO; GO:0009897; C:external side of plasma membrane; IDA.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0005764; C:lysosome; IDA.  
 DR GO; GO:0042613; C:MHC class II protein complex; IDA.  
 DR GO; GO:0045012; F:MHC class II receptor activity; IDA.  
 DR GO; GO:0042605; F:peptide antigen binding; IDA.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR GO; GO:004591; P:antigen presentation, exogenous antigen via. .; IDA.  
 DR GO; GO:0048005; P:antigen presentation, exogenous peptide ant. .; IDA.  
 DR GO; GO:0045582; P:positive regulation of T-cell differentiation; IDA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR001003; MHC II\_alpha.  
 DR Pfam; PF07654; C1-set; 1\_alpha.  
 DR Pfam; PF00993; MHC\_II\_alpha; 1.  
 DR SMART; SM00407; IGC1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
 SQ SEQUENCE 256 AA; 28158 MW; DDBBAA26D74219E CRC64;

Alignment Scores:  
 Pred. No.: 1,54e-72 Length: 256  
 Score: 1107.00 Matches: 205  
 Percent Similarity: 94.98% Conservative: 3  
 Best Local Similarity: 93.61% Mismatches: 11  
 Query Match: 41.08% Indels: 0  
 DB: 2 Gaps: 0

US-10-048-116-1 (1-1484) x Q8K2X0 (1-256)

QY 1 ATGCGGTGACGAGAGCTGATTCTGGGGTCTCGCCCTGAACACCATGCTCAGCCTC 60  
 DB 1 MetProCysSerArgAlaLeuLeuLeuGlyValLeuAlaLeuAnThrMetLeuSerLeu 20  
 QY 61 TGGGAGGTGAAGACGACATTGAGGCGCCAGCCAGCTAGGCTTCTATGGTACAACTGTTTAT 120  
 DB 21 CysGlyGlyGluAspValIleGluAlaAspHisValGlyPheTyrGlyIleValTyr 40  
 QY 121 CAGTCTCTGAGACATGCGCCAGTACACATGAATTTGATGGTGTGATGTTGTTCTAT 180  
 DB 41 GlnSerProGlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyrPheTyr 60  
 QY 181 GTGGACTTGTGATAAGAAAGAACTGCTGGAGGCTTCTCAGTGTGGCCAAATGATGACTC 240  
 DB 61 ValAspLeuAspIlySylThrValTyrMetLeuProGluPheGlyGlnLeuLeuSer 80  
 QY 241 TTGTAGCCCCAAGTGGAGCTGCAAAACATAGCTGCAGAAAAACACAACTTGGGAATCTTG 300  
 DB 81 PheAspProGlnGlyGlyLeuGlnAenIleAlaThrGlyLysHisAenLeuGlyTyr 100  
 QY 301 ACTAAGAGTCAATTTCCACCCAGCTACCAATGAGGCTCTCTCAAGGACTGTGTTCCCC 360  
 DB 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120

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Qy 361 AAGTCCCTGCTGCTGGTGCAGCCCAACACCTTATCTGCTTTGTGGACAACATCTTC 420
Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140
Qy 421 CCACCTGTGATCAACATCACATGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480
Db 141 ProProValIleAsnIleThrTriPLeuArgAsnSerLysSerValThrAspGlyValTyr 160
Qy 481 GAGACCACTCTCTGCTGCAACCGTGACCATCTCTTCCAAAGCTGTCTTATCTCACCTTC 540
Db 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180
Qy 541 ATCCCTCTGATGATGACATTATGACTGCAAGGTGGAGCACTGGCGCTGGAGAGCGC 600
Db 181 IleProSerAspAspIleTyrAspCysLysValGluHisTrpGlyLeuAspGluPro 200
Qy 601 GTTCTGAACACTGGGAACCTGAGATTCACGCCCTCATGTCCAGAGCTGCACAGAACT 657
Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219

RESULT 11
Q860C1 PRELIMINARY; PRT; 256 AA.
AC Q860C1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similar to histocompatibility 2, class II antigen A, alpha.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L.H., Schuler G.D.,
RA Klausner R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP [2]
RC SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC043925; AA043925.1; -.
DR HSSP; P01910; 1D9K.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001003; MHC_II_alpha.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00993; MHC_II_alpha; 1.

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Qy 121 CAGTCTCTCGAGACATTGGCCAGTACACATCAATTTGATGCTGATGATGTTCTTCTAT 180
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Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219

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DT 01-JAN-1990 (Rel. 13, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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DE (TAaapha).
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OS Mus musculus (Mouse).
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RN SEQUENCE FROM N.A.  
 RP Rowen L., Qin S., Ahearn M.E., Loretz C., Faust J., Lasky S.,  
 RA Mahairas G., Hood L.E.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
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 RN SEQUENCE FROM N.A.  
 RP Rowen L., Qin S., Loretz C., Mix L., Lasky S., Madan A., Hood L.E.;  
 RA "Sequence of the mouse major histocompatibility class II region.";  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
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 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
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 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
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 RN SEQUENCE OF 9-256 FROM N.A.  
 RP MEDLINE=83285339; PubMed=6309407; DOI=10.1016/0092-8674(83)90147-2;  
 RA Benoist C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;  
 RT "Regions of allelic hypervariability in the murine A alpha immune  
 response gene";  
 RL Cell 34:169-177(1983).  
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 DR EMBL; AF050157; AAC05285.1; -  
 DR EMBL; BC019721; AAH19721.1; -  
 DR EMBL; BC031711; AAH31711.1; -  
 DR EMBL; K01922; AAA39614.1; -  
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 DR PDB; 1MUJ; X-ray; A=24-219.  
 DR MGD; MGI:95895; H2-Aa.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001003; MHC\_II\_alpha.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00993; MHC\_II\_alpha; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
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 FT DOMAIN 24 111 Extracellular alpha-1.  
 FT DOMAIN 112 205 Extracellular alpha-2.  
 FT DOMAIN 206 218 Connecting peptide.  
 FT TRANSMEM 219 244

FT DOMAIN 245 256 Cytoplasmic tail.  
 FT DISULFID 134 190 By similarity.  
 FT CARBOHYD 145 145 N-linked (GlcNAc...) (Potential).  
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 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE H-2 class II histocompatibility antigen, A-K alpha chain precursor.  
 GN Name=H2-Aa;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 RX MEDLINE=8314188; PubMed=3137158;  
 RA Bishop G.A., McMillan M.S., Houghton G., Frelinger J.A.;  
 RT "Signaling to a B-cell clone by Bk, but not Ak, does not reflect  
 RL alteration of Ak genes."; Immunogenetics 28:184-192(1988).  
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 RP SEQUENCE OF 4-256 FROM N.A.  
 RX MEDLINE=83169693; PubMed=6300851;  
 RA Benoit C.O., Mathis D.J., Kanter M.R., Williams V.E., McDevitt H.O.;  
 RT "The murine Ia alpha chains, E alpha and A alpha, show a surprising  
 RL degree of sequence homology."; Proc. Natl. Acad. Sci. U.S.A. 80:534-538(1983).  
 RN [3]  
 RP SEQUENCE OF 24-256 FROM N.A.  
 RX MEDLINE=8519610; PubMed=2581258;  
 RA Landais D., Matthes H., Benoit C., Mathis D.;  
 RT "A molecular basis for the Ia.2 and Ia.19 antigenic determinants."; Proc. Natl. Acad. Sci. U.S.A. 82:2930-2934(1985).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 27-208.  
 RX MEDLINE=98187997; PubMed=9529148; DOI=10.1016/S1074-7613(00)80536-1;  
 RA Fremont D.H., Monnaie D., Nelson C.A., Hendrickson W.A., Unanue E.R.;  
 RT "Crystal structure of I-Ak in complex with a dominant epitope of  
 RL lysozyme."; Immunity 8:305-317(1998).  
 CC -----  
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 DR EMBL; M21931; AAA39636.1; -;  
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 DR InterPro; IPR003597; Ig cl.  
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 DR Pfam; PF00047; ig; 1.  
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 DR SMART; SM00407; IGCL; 1.  
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 DB 201 ValLeuLysHisTyrPheGluProGluIleProAlaProMetSerGluLeuThrGluThr 219









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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 16, 2005, 01:40:32 ; Search time 60 Seconds  
(without alignments)

4759.523 Million cell updates/sec

Title: US-10-048-116-1

Perfect score: 2695

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Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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Database :

PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1319.5	49.0	469	2	S37483
2	1317	48.9	446	2	S40295
3	1313.5	48.7	330	1	G2M5A
4	1313.5	48.7	399	1	G2M5AM
5	1182	43.9	256	1	HLMSA2
6	1075	39.9	256	2	I14447
7	1075	39.9	258	1	HLMSAA
8	1057	39.2	254	2	S11649
9	1037	38.5	335	1	G2M5BM
10	1012.5	37.6	405	1	G2M5B1
11	1010	37.5	474	1	G2M511
12	1006	37.3	475	2	S01321
13	1000	37.1	233	2	I79357
14	996	37.0	233	2	I79358

ALIGNMENTS

RESULT 1

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submitted to the EMBL Data Library, February 1993  
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A;Residues: 1-469 <DUC>  
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
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US-10-048-116-1 (1-1484) x S37483 (1-469)

QY	100	TTCTATGGTACACATGTTTATCAGTCTCTCTGGAGAC-----ATTGGC-----	141
DB	51	TyrTyrIleAsnTrpVallysGlnLysProGlyLeuLysTrpIleGlyTrpIle	70
QY	142	-----CAGTACACACATGAATTTGATCGTCATGAGTTGTTCTAT	180
DB	71	TyrProAlaSerGlyAsnThrLysTyrAsnGluAsnPhenylsGlyAlaThrLeuThr	90
QY	181	GTGGACTTGGATAAGAAGAAACTGTCTGGAGCTTCCTGAGTTT-----	225

91	valAspThrSerSerSerThrAlaTyrMetGlnLeuSerSerLeuThrSerGluAspThr	110
226	-----GGCCAAATTGATACCTCTTTGAGCCC	249
111	AlaValTyrPheCysAlaArgAlaMetGlyAlaThrAlaThrLeuLeuAspTyrTrpGly	130
250	CAAGGTGGACTGGAAAAACATAGCTGCAGAAAAACACAACCTTGGAAATCTTGACTAAGAGG	309
131	GlnGlyThrThrLeuThrValSerSerAlaLys	141
310	TCAAAATTCACCCAGCTACCAATGAGGCTCCTCAAGGAGCTGTGTCCCAAGTCGCCCT	369
142	-----ThrThrAlaPro-----SerValTyrProLeuAlaPro	152
370	GTG-----CTGCTGGGTGACGCCCAACACCTTATCTGCTTGTGGACAACATCTTC	420
153	ValCysGlyAspThrThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPhe	172
421	CCACCTGTGATCAACATCACATGCTCAGAAATAGCAAGTCAGTCACAGACGGGTTCAT	488
173	ProGluProValThrLeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal	189
481	GAGACCAAGCTTCCTCGTCAACCGTGACATTCCTTCCACAAGCTGTCTTATCTCACCTTC	540
190	-----HisThrPheProAlaVal-----	195
541	ATCCCTCTTGATGATGACATTTATGACTGC AAGGTGGAGCACTGGGCGCTGGAGGAGCGG	600
196	-----LeuGlnSerAspLeuTyrThrLeuSer	204
601	GTTCTGAAACACATGGGAACTGAGATTCAGCCCCCATGTGCAGAGCTCAGACAAACTGGA	660
205	-----SerSerValThrValThr-----	210
661	GGTGGAGATCCATACAGCTCCATCAGCTCAGCTCGCAAAAAGAGCTCCAGGCGCTGGAG	720
211	-----SerSerThr-----	213
721	AAGGAAAAATGCACAGCTGGAATGGAGTGTGCAAGCACTGGAAAAAGGAACCTGGCTCAGGCA	780
214	-----TrpProSerGlnSerIleThrCysAsnValAlaIlePro	226
781	GCATCT-----GAGCCACAGAGCGGCCCAACAATCAAGCCCTGT	816
227	AlaSerSerThrLysValAspLysLysIleGluProArgGlyProThrIleLysProCys	246
817	CTCTCCATGCAAAATGCCAGACCACTCACTCTGGGTGGACCAATCCGCTTCATCTCCCT	876
247	ProProCysLysCysProAlaProAsnLeuLeuGlyGlyProSerValPheIlePhePro	266
877	CCAAAGATCAAGGATGACTCATGATCTCCCTGAGCCCACTAGTCACATGTGTGGTGGT	936
267	ProLysIleLysAspValLeuMetIleSerLeuSerProIleValThrCysValValVal	286
937	GATGTGAGCAGATGATGATCCAGATGTCCAGATCAGCTGGTTGTGGAACAACCTGGAAGTA	996
287	AspValSerGluAspAspProAspValGlnIleSerTrpPheValAsnAsnValGluVal	306
997	CACACAGCTCAGACACAAACCATAGAGAGATTAACAACAGTACTCTCCGGGTGGTCAGT	1056
307	HisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSer	326
1057	GCCTCCCCCATCAGCACACGAGCTGATGATGGCAGAGGATTCAAATCCAGGTCAAC	1116
327	AlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsn	346
1117	AACAAAGACCTCCACAGCGCCCATCGACAGAACCATCTCAAAACCCCAAGGCTCAGTAAGA	1176
347	AsnLysAspLeuProAlaProIleGluArgThrIleSerLysProLysGlySerValArg	366
1177	GTCTCCAGGTATATGTCTTCCTCCACAGAGAGAGATGACTAAGAACAGGTCACT	1236
367	AlaProGlnValTyrValLeuProProGluGluMetThrLysLysGlnValThr	386

Qy	1237	CTGACCTGCATGGTTCACAGACTTCATGCCTGGAAGACATTTACCTGGAGTGGACCAACAAC	1239
Db	387	LeuThrCysMetValThrAspPheMetProGluAspIleTyrValGluTprThrAsnAsn	406
Qy	1297	GGGAAACACAGAGCTAAACTACAAGACACTGAACACCTGGCTGGAAAGAACTAGCTACTCTTAC	1356
Db	407	GlyLysThrGluLeuAsenTyrLysAsnThrGluProValLeuAspSerAspGlySerTyr	426
Qy	1357	TTCATGTATGACGACGCTGAGAGTGGGAAAGAACTGGGTGGAAAGAAATAGCTACTCTCC	1416
Db	427	PheMetTyrSerLysLeuArgValGluLysLysAsnTprValGluArgAsnSerTyrSer	446
Qy	1417	TGTTACAGTGTGCACGAGGGCTGTGCACAATCACACACGACTAAGAGCTTCTCCCGGACT	1476
Db	447	CysSerValValHisGluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThr	466
Qy	1477	CCGGGT 1482	
Db	467	ProGly 468	
RESULT 2			
S40295			
Ig gamma-2a chain (mab735) - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004			
C:Accession: S40295			
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaessen, M.; Frosch, M.; Weisgerber			
submitted to the EMBL Data Library, January 1993			
A:Description: Primary structure of the murine monoclonal IgG2a antibody mab735			
A:Reference number: S40295			
A:Accession: S40295			
A:Molecule type: protein			
A:Residues: 1-446 <KLE>			
A:Cross-references: UNIPROT:Q99L25			
C:Genetics:			
A:Map position: 12			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglytamic acid			
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>			
F:1-117/Domain: V-D-J region <VDJ>			
F:118-446/Domain: C region <CHR>			
F:118-214/Domain: C1 region <CH1>			
F:215-230/Region: hinge			
F:231-340/Domain: C2 region <CH2>			
F:341-446/Domain: C3 region <CH3>			
F:360-427/Domain: immunoglobulin homology <IMM>			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted			
F:132/Disulfide bonds: interchain (to light chain) #status predicted			
F:224,227,229/Disulfide bonds: interchain #status predicted			
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental			
Alignment Scores:			
Pred. No.:	3,75e-84	Length:	446
Score:	1317.00	Matches:	280
Percent Similarity:	63.52%	Conservative:	30
Best Local Similarity:	57.38%	Mismatches:	78
Query Match:	48.8%	Indels:	100
DB:	2	Gaps:	12
US-10-048-116-1 (1-1484) x S40295 (1-446)			
Qy	100	TTCTATGGTTCACACTGTTTATCATGCTCTCTGGAGAC-----ATTGGC-----	141
Db	32	TyrTyrIleHisTprValLysGlnArgProGlyGluGlyLeuGluTprIleGlyTprIle	51
Qy	142	-----CAGTACACACATGAATTTGATGGTGATGATGTTTCTAT	180
Db	52	TyrProGlySerGlyAsnThrLysTyrAsnGluLysPheLysGlyLysAlaThrLeuThr	71
Qy	181	GTGACTTGGATGAAGAAACTGTCTGGAGGCTTCTGGAGTTT-----GGCCAA	231

Db 72 ValAspThrSerSerSerThrAlaTyMetGlnLeuSerSerLeuThrSerGluAspSer 91  
QY 232 TTGATACTCTTTGAGCCCAAGGTGGACTGCAAAACATAGCTGCAGAAAACACAACTTG 291  
Db 92 AlavalTyPheCysAlaArgGlyGly- 104  
QY 292 GGAATCTTGATGAAGAGGTCAAAATTTCCACCCAGCTACCAATAGAGCTCTCTCAAGGACT 351  
Db 105 AspTy-TripGlyGlnGlyThrSerValThrValSerSerAlaLysThrThrAlaProSer 124  
QY 352 GTGTTCCCCAGTCCCTCTGTG-----CTGCTGGTCCAGCCCAACACCTTATCTGTC 402  
Db 125 ValTy-ProLeuAlaProValCysGlyAspThrThrGlySerSerValThrLeuGlyCys 144  
QY 403 TTTGTGACAAACATCTTCCACCTGTGATCAACATCACATGGCTCAGAAATACCAAGTCA 462  
Db 145 LeuValLysGlyTyPheProGluProValThrLeuThrTrp-----AsnSerGlySer 162  
QY 463 GTCACAGACGGCGTTTATGAGACACAGCTTCTCTCAACCGTGACCATTCCTTCCACAAG 522  
Db 163 LeuSerSerGlyVal-----HisThrPheProAla 172  
QY 523 CTGCTTATCTACCTTCATCCCTTCTGATGATGACATTTATGACTGCAAGGTGGAGCAC 582  
Db 173 Val-----LeuGlnSerAspLeuTyThrLeuSer----- 182  
QY 583 TGGGGCTGGAGGAGCGGTTCTGAAACACTGGGAACCTGAGATTCAGCCCCCATGTCA 642  
Db 183 -----Ser 183  
QY 643 GAGCTGACAGAAACTGGAGGTGGAGGATCCATCAGCTCAGCTCGAAAAA 702  
Db 184 SerValThrValThr-----SerSerThr----- 191  
QY 703 GAGCTCAGGCCCTGGAGAAGGAAAATGCACAGCTGGAATGGAGTTGCAGACACTGGAA 762  
Db 192 -----TrpProSerGlnSerIleThr 198  
QY 763 AAGGAACGTGCTCAGGCAGCATCT-----GAGCCACAGGG 798  
Db 199 CysAsnValAlaHisProAlaSerSerThrLysValAspLysLysIleGluProArgGly 218  
QY 799 CCACAAATCAAGCCCTGTCTCTCCATGCAATGCCAGCACCTTAACCTCTTGGGTGGACCA 858  
Db 219 ProThrIleLysProCysProCysProLysCysProAlaProAsnLeuLeuGlyGlyPro 238  
QY 859 TCGCTCTTCATCTTCCCTCAAGATCAAGGATGTACTATGATCTCCCTGAGCCCCATA 918  
Db 239 SerValPheIlePheProProLysIleLysAspValLeuMetIleSerLeuSerProMet 258  
QY 919 GTCACATGTGTGTGGTGTGATGAGCGAGGATGACCCAGATCTCCAGATCAGCTCGTTT 978  
Db 259 ValThrCysValValValAspValSerGluAspAspProAspValGlnIleSerTrpPhe 278  
QY 979 GTGAACAAACGTGAAGTACACAGCTGCAGACAAACCCATAGAGAGGATTAACAAGT 1038  
Db 279 ValAsnAsnValGluValLeuThrAlaGlnThrGlnThrHisArgGluAspTyAsnSer 298  
QY 1039 ACTCTCGGGTGTGATGTCAGTCCCTCCCATCCAGACACAGACTGGATGAGTGCAGAGGAG 1098  
Db 299 ThrLeuArgValValSerAlaLeuProIleGlnHisGlnAspTrpMetSerGlyLysGlu 318  
QY 1099 TTCAATGCAAGTCAACAAAGACCTCCAGCGCCCATCCAGAGAACCATCTCAAAA 1158  
Db 319 PheLysCysLysValAsnAsnLysAspLeuProAlaProIleGluArgThrIleSerLys 338  
QY 1159 CCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGCTCTTGCTCCACAGAGAAGAGATG 1218  
Db 339 ProLysGlySerValArgAlaProGlnValTyValLeuProProGluGluGluMet 358  
QY 1219 ACTAAGAAACAGTCTCTGACTGATGGTGCAGACTTTCATGCTGAAGACATTAC 1278  
Db 359 ThrLysLysGlnValThrLeuThrCysMetValThrAspPheMetProGluAspIleTy 378

QY 1279 GTGGAGTGGACCAACAAACGGAACACAGAGCTAAACTACAAGAACTGAAACAGTCCTG 1338  
Db 379 ValGluTrpThrAsnAsnGlyLysThrGluLeuAsnTyLysAsnThrGluProValLeu 398  
QY 1339 GACTCTGATGGTCTTACTTACATGATACAGAGCTGAGAGTGAAGAAAGAACTGGGTG 1398  
Db 399 AspSerAspGlySerTyPheMetTySerLysLeuArgValGluLysAsnTrpVal 418  
QY 1399 GAAGAAATAGCTACTCTCTGTTTCAGTGGTCCAGAGGTCGCACAAATCACACACAGACT 1458  
Db 419 GluArgAsnSerTySerCysSerValValHisGluGlyLeuHisAsnHisIleThrThr 438  
QY 1459 AAGAGCTTCTCCCGGACTCCGGGT 1482  
Db 439 LysSerPheSerArgThrProGly 446  
RESULT 3  
G2MSA  
IG gamma-2a chain C region, secreted form (allele a) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1980 #sequence revision 01-Sep-1981 #text\_change 09-Jul-2004  
C:Accession: A02152; A32657; A32658  
R:Sikorav, J.L.; Auffray, C.; Rougeon, F.  
Nucleic Acids Res. 8, 3143-3155, 1980  
A:Title: Structure of the constant and 3' untranslated regions of the murine Balb/C gamma  
A:Reference number: A02152; MUID:81076554; PMID:6777755  
A:Accession: A02152  
A:Molecule type: mRNA  
A:Residues: 1-330 <SIK>  
A:Cross-references: UNIPROT:P01863; GB:V00798; NID:G51835; PIDN:CAA24178.1; PID:gl3333984  
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.  
Nucleic Acids Res. 9, 1365-1381, 1981  
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol  
A:Reference number: A32657; MUID:81198976; PMID:6262729  
A:Accession: A32657  
A:Molecule type: DNA  
A:Residues: 1-330 <YAM>  
A:Cross-references: GB:J00470  
A:Note: the sequence was determined from the germline gene  
R:Ollo, R.; Auffray, C.; Morthams, C.; Rougeon, F.  
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981  
A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests t  
A:Reference number: A32658; MUID:81223894; PMID:6787604  
A:Accession: A32658  
A:Molecule type: DNA  
A:Residues: 1-330 <OLL>  
A:Note: the sequence was determined from the germline gene  
A:Note: Lys-330 is removed posttranslationally  
R:Boutgeois, A.; Fougereau, M.; Rocca-Serra, J.  
Eur. J. Biochem. 43, 423-435, 1974  
A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-ac  
A:Reference number: A32659; MUID:74175517; PMID:4831970  
A:Contents: annotation; myeloma protein MOPC 173  
A:Note: this is one paper in a series reporting the sequence; for additional references,  
R:de Preval, C.; Fougereau, M.  
Eur. J. Biochem. 30, 452-462, 1972  
A:Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. Ident  
A:Reference number: A32660; MUID:73056887; PMID:4565406  
A:Contents: annotation; MOPC 173, disulfide bonds  
C:Genetics:  
A:Introns: 1/1; 98/1; 114/1; 224/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa  
chain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into lai  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul  
F:20-84/Domain: immunoglobulin homology <IM1>  
F:98-113/Region: hinge  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:15/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-82,144-204,250-308/Disulfide bonds: #status experimental

F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 6,42e-84 Length: 330  
Score: 1313.50 Matches: 267  
Percent Similarity: 71.03% Conservative: 15  
Best Local Similarity: 67.25% Mismatches: 36  
Query Match: 48.74% Indels: 79  
DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x G2MSA (1-330)

QY	325	GCTACCAATGAGCTCTCAAGCAGCTGTGTTCCTCCCAAGTCCCTGTG-----CTG	375
DB	1	AlaLysThrThrAlaPro-----SerValTyrProLeuAlaProValCysGlyAspThr	18
QY	376	CTGGGTGAGCCCAACACCTTATCTGCTTTGTGGACAACATCTTCCACCTGTGATCAAC	435
DB	19	ThrGlySerSerValThrLeuGlyCysLeuValLysGlyTyrPheProGluProValThr	38
QY	436	ATCACATGGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTATGAGACCAGCTTCCTC	495
DB	39	LeuThrTrp-----AsnSerGlySerLeuSerSerGlyVal-----	50
QY	496	GTCACCGTGACCATTCCTTCCACAGCTGTCTTATCTCACCTTCATCCCTTCGTGATGAT	555
DB	51	-----HisThrPheProAlaVal-----LeuGlnSer	59
QY	556	GACATTTATGACTGCAAGGTGGACACTGGGGCTGGAGGAGCGGTTCTGAAACACTGG	615
DB	60	AspLeuTyrThrLeuSer-----	65
QY	616	GAACCTGAGATTCCAGCCCTCATGCTCAGAGCTGACAGAACTGGAGGTGGAGTCCACT	675
DB	66	-----SerSerValThrValThr-----SerSer	73
QY	676	ACAGCTCAGTCACTCAGCTCGAANAAGAGCTCCAGGCCCTGGAGAGGAAATGCAAG	735
DB	74	Thr-----	74
QY	736	CTGGAATGGGAGTTGCAAGCACTGGAAAGAACTGGCTCAGGCAGCATCT-----	786
DB	75	-----TrpProSerGlnSerIleThrCysAsnValAlaHisProAlaSerThrLys	92
QY	787	-----GAGCCAGAGGGCCCCAATCAAGCCCTGCTCTCCATGCAAAATGC	831
DB	93	ValAspLysIleGluProArgGlyProThrIleLysProCysProProCysLysCys	112
QY	832	CCAGCACTAACCTCTTGGGTGGACCATCGCTCTTCATCTTCCCTCCAAAGATCAAGAT	891
DB	113	ProAlaProAsnLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp	132
QY	892	GTACTCATGATCTCCCTGAGCCCATAGTCACATGTGTGGTGGATGTGAGCGAGAT	951
DB	133	ValLeuMetIleSerLeuSerProIleValThrCysValValValAspValSerGluAsp	152
QY	952	GACCCAGATGCCAGATCAGCTGGTTGTGTGAACACGTGGAGGTACACAGCTCAGACA	1011
DB	153	AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr	172
QY	1012	CAAAACCATAGAGAGGATTACAAAGTACTCTCCGGTGTGTCAGTGCCTCCCATCCAG	1071
DB	173	GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln	192
QY	1072	CACGAGACTGGATGAGTGGCAAGGAGTTCAATGCAAGGTCAACAAAGACTCCCA	1131
DB	193	HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnLysAspLeuPro	212
QY	1132	CGGCCCATCGAGAAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATAT	1191
DB	213	AlaProIleGluArgThrIleSerLysProLysGlySerValArgAlaProGlnValTyr	232

QY	1192	GTCTTGCTCCACCAGAAAGAGAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTC	1251
DB	233	ValLeuProProProGluGluMetThrLysLysGlnValThrLeuThrCysMetVal	252
QY	1252	ACAGACTTCATGCTGAAGACATTTACGTGGAGTGGACCAACAAACGGGAAACAGAGCTA	1311
DB	253	ThrAspPheMetProGluAspIleTyrValGluTrpThrAsnAsnGlyLysThrGluLeu	272
QY	1312	AACTACAAAGAACACTGAACAGCTCCTGGACTCTGATGGTTCTTACTTTCATGTACAGCAAG	1371
DB	273	AsnTyrLysAsnThrGluProValLeuAspSerAspGlySerTyrPheMetTyrSerLys	292
QY	1372	CTGAGAGTGAAGAAGAACTGGGTGGAAGAAATAAGTACTCTCTTTCAGTGTGTCAC	1431
DB	293	LeuArgValGluLysLysAsnTrpValGluArgAsnSerTyrSerCysSerValValHis	312
QY	1432	GAGGTCTGCACATCAACACAGCACTAAGAGCTTCTCCCGGACTCCGGGT	1482
DB	313	GluGlyLeuHisAsnHisHisThrThrLysSerPheSerArgThrProGly	329

RESULT 4

G2MSAM  
IG gamma-2a chain C region, membrane-bound form - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 19-Feb-1984 #sequence\_revision 31-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: A02154; B32657; I57809  
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.  
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982  
A:Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul  
A:Reference number: A02154; MUID:82222190; PMID:6283537  
A:Accession: A02154  
A:Molecule type: DNA  
A:Residues: 329-399 <YAM>  
A:Cross-references: UNIPROT:P01865; GB:J00471  
A:Note: The sequence was determined from the germline gene  
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.  
Nucleic Acids Res. 9, 1365-1381, 1981  
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and ev  
A:Reference number: A32657; MUID:81198976; PMID:6262729  
A:Accession: B32657  
A:Molecule type: DNA  
A:Residues: 1-329 'K' <YA2>  
R:Hall, B.; Milcarek, C.  
Mol. Immunol. 26, 819-826, 1989  
A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin ga  
A:Reference number: I57809; MUID:90097953; PMID:2513486  
A:Accession: I57809  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 373-399 <RES>  
A:Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217  
C:Comment: The sequence of residues 1-328 was assumed to be identical with the correspond  
C:Comment: Cell lines producing IGG contain two mRNA species for Ig gamma chains. The ma  
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit  
C:Genetics:  
C:Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
F:137-206/Domain: immunoglobulin homology <IMM>  
F:346-363/Domain: transmembrane #status predicted <TM>  
F:364-399/Domain: intracellular #status predicted <INT>  
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 6,52e-84 Length: 399  
Score: 1313.50 Matches: 267  
Percent Similarity: 71.03% Conservative: 15  
Best Local Similarity: 67.25% Mismatches: 36  
Query Match: 48.74% Indels: 79  
DB: 1 Gaps: 9



QY 301 ACTAAGAGGTCAAAATTTCAACCCAGCTACCAATGAGGCTCCTCAAGCAGCTGTGTTCCCC 360  
 Db 101 ThrLysArgSerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120  
 QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACCTTATCTCTTGTGGCAACATCTTC 420  
 Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuLeuCysPheValAspAsnIlePhe 140  
 QY 421 CCACCTGTGATCAACATCAGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480  
 Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160  
 QY 481 GAGACCACTCTCTGCTCAACCGTGACCATTCCTTCCACAGCTGCTTATCTCAGCTTC 540  
 Db 161 GluThrSerPheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPhe 180  
 QY 541 ATCCCTCTGATGATGACATTTATGACTGCAAGGTGAGCACTGGGCGCTGGAGAGCGG 600  
 Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200  
 QY 601 GTTCTGAAACACTGGGAACCTGAGATTCACGCCCCCATGTGACAGCTGACAGAACT 657  
 Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219  
 RESULT 6  
 154447  
 Gene MHC H2-I-A-alpha chain protein - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: I54447  
 R:Bishop, G.A.; McMillan, M.S.; Houghton, G.; Frelinger, J.A.  
 Immunogenetics 28, 184-192, 1988  
 A:Title: Signaling to a B-cell clone by E-k, but not A-k, does not reflect alteration of  
 A:Reference number: I54447; MUID:88314188; PMID:3137158  
 A:Accession: I54447  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-256 <RES>  
 A:Cross-references: UNIPROT:P01910; GB:M21931; NID:g199493; PIDN:AAA39636.1; PID:g199494  
 C:Genetics:  
 A:Gene: MHC-H2-I-A-alpha  
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology  
 F:127-192/Domain: immunoglobulin homology <IMM>  
 Alignment Scores:  
 Pred. No.: 2,75e-67 Length: 256  
 Score: 1075.00 Matches: 203  
 Percent Similarity: 93.61% Conservative: 2  
 Best Local Similarity: 92.69% Mismatches: 14  
 Query Match: 39.89% Indels: 0  
 DB: 2 Gaps: 0  
 US-10-048-116-1 (1-1484) x I54447 (1-256)  
 QY 1 ATGCCGTGCACGACGCTCTGATTCGGGGTCTCGCCCTGACACCATGCTCAGCCTC 60  
 Db 1 MetBroArgSerArgAlaLeuIleGlyValLeuAlaLeuThrMetLeuSerLeu 20  
 QY 61 TGGCGAGGTGAAGACGACATTCAGGCGCCACCATGAGCTTCTATGCTACAACTGTTTAT 120  
 Db 21 CysGlyGlyGluAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyr 40  
 QY 121 CAGTCTCTGAGACATTTGGCCAGTACACATGAATTTGATGTGATGAGTGTCTTCTAT 180  
 Db 41 GlnSerProGlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyr 60  
 QY 181 GTGCACCTGGATAGAAGAAATGCTGGAGGCTCTCTGAGCTTGGCCAAATGATCATC 240  
 Db 61 ValAspLeuAspLysLysGluThrValTrpMetLeuProGluPheAlaGlnLeuArg 80  
 QY 241 TTTGAGCCCCAAGGTGAGCTGCAAAACATAGCTGCAGAAACACAACTTTGGGAATCTTG 300  
 Db 81 PheGluProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGluIleLeu 100

QY 301 ACTAAGAGGTCAAAATTTCAACCCAGCTACCAATGAGGCTCCTCAAGCAGCTGTGTTCCCC 360  
 Db 101 ThrLysArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPhePro 120  
 QY 361 AAGTCCCTGCTGCTGGGTGAGCCCAACACCTTATCTCTTGTGGCAACATCTTC 420  
 Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuLeuCysPheValAspAsnIlePhe 140  
 QY 421 CCACCTGTGATCAACATCAGCTCAGAAATAGCAAGTCAGTCACAGACGGCGTTTAT 480  
 Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyr 160  
 QY 481 GAGACCACTCTCTGCTCAACCGTGACCATTCCTTCCACAGCTGCTTATCTCAGCTTC 540  
 Db 161 GluThrSerPheValAsnArgAspTyrSerPheHisLysLeuSerTyrLeuThrPhe 180  
 QY 541 ATCCCTCTGATGATGACATTTATGACTGCAAGGTGAGCACTGGGCGCTGGAGAGCGG 600  
 Db 181 IleProSerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluGluPro 200  
 QY 601 GTTCTGAAACACTGGGAACCTGAGATTCACGCCCCCATGTGACAGCTGACAGAACT 657  
 Db 201 ValLeuLysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 219  
 RESULT 7  
 HLMSAA  
 H-2 class II histocompatibility antigen A alpha chain - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1985 #sequence\_revision 25-Feb-1985 #text\_change 09-Jul-2004  
 C:Accession: A02217, I59023; A32510  
 R:Benoist, C.O.; Mathis, D.J.; Kanter, M.R.; Williams II, V.B.; McDevitt, H.O.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 534-538, 1983  
 A:Title: The murine Ia alpha chains, E-alpha and A-alpha, show a surprising degree of se  
 A:Reference number: A93967; MUID:83169693; PMID:6300851  
 A:Accession: A02217  
 A:Molecule type: mRNA  
 A:Residues: 1-258 <BEN>  
 A:Cross-references: UNIPROT:P01910  
 A:Experimental source: clone pAAC6  
 R:Landais, D.; Matthes, H.; Benoist, C.O.; Mathis, D.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 2930-2934, 1985  
 A:Title: A molecular basis for the Ia.2 and Ia.19 antigenic determinants.  
 A:Reference number: I59023; MUID:85190610; PMID:2581258  
 A:Accession: I59023  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 26-258 <RES>  
 A:Cross-references: GB:M11357; NID:g199445; PIDN:AAA39613.1; PID:g387459  
 R:Sharma, S.; King, L.B.; Corley, R.B.; Maki, R.  
 Immunol. Invest. 16, 425-436, 1987  
 A:Title: Comparative sequence analysis of cDNA clones encoding I-A molecules of the CH12  
 A:Reference number: A91752; MUID:88085327; PMID:3500915  
 A:Accession: A32510  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 18-258 <SHA>  
 C:Comment: Residues 1-25 are part of the signal sequence.  
 C:Comment: Residues 26-113, 114-207, and 208-258 are the first and second extracellular  
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology  
 C:Keywords: glycoprotein; heterodimer; transmembrane protein  
 F:129-194/Domain: immunoglobulin homology <IMM>  
 F:136-192/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Alignment Scores:  
 Pred. No.: 2,76e-67 Length: 258  
 Score: 1075.00 Matches: 202  
 Percent Similarity: 94.01% Conservative: 2  
 Best Local Similarity: 93.09% Mismatches: 13  
 Query Match: 39.89% Indels: 0  
 DB: 1 Gaps: 0



US-10-048-116-1 (1-1484) x HLMSAA (1-258)

QY 7 TGAGAGAGAGCTCTGATTCTGGGGTCTCGCCTGAACACCATGCTCAGCCTCTGGGA 66  
Db 5 CysSerArgAlaLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeuCysGly 24  
QY 67 GGTGAAGACGACATTGAGCGCGACCGTAGGTCTTATGGTACAACTGTTTATCAGTCT 126  
Db 25 GlyGluAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyrGlnSer 44  
QY 127 CTGGGACACATTCGCCAGTACACACATGAATTTGATGGTATGAGTCTTCTATGGAC 186  
Db 45 ProGlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyrValAsp 64  
QY 187 TTGGATAAGAAAGAACTCTGGAGGCTTCTGAGTTTGGCCAAATTGATCTTTGAG 246  
Db 65 LeuAspLysGlyGlnThrValTrpMetLeuProGluPheAlaGlnLeuArgArgPheGlu 84  
QY 247 CCCAAGGTGGATGCAAAATAGCTGCAGAAAAACACAACTTGGGAATCTTTGACTAAG 306  
Db 85 ProGlnGlyGlyLeuGlnAsnIleAlaThrGlyLysHisAsnLeuGluIleLeuThrLys 104  
QY 307 AGCTCAAAATTCACCCAGTACCAATGAGGCTCTCAAGCGACTGTGTTCCCAAGTCC 366  
Db 105 ArgSerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSer 124  
QY 367 CTGTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGACAACTTTCCACCT 426  
Db 125 ProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProPro 144  
QY 427 GTGATCAACATCATGGCTCAGAAATAGCAAGTCAGTCAAGCGCGGTTTATGAGACC 486  
Db 145 ValIleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThr 164  
QY 487 AGCTTCTCTGCAACGTCAGCAATCTTCCACAGCTGCTTATCTCAGCTTCATCCCT 546  
Db 165 SerPhePheValAsnArgAspTyrSerPheHisLysLeuSerTyrLeuThrPheIlePro 184  
QY 547 TCTGATGATCAGATTTATGACTCAAGGTGAGCACTGGGGCTGGAGGAGCGGTTCTG 606  
Db 185 SerAspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeu 204  
QY 607 AAACACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAACT 657  
Db 205 LysHisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 221

RESULT 8  
S11649  
class II histocompatibility antigen H-2-I-A-alpha NON - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: I48421; S11649  
R;Acha-Orbea, H.; Scarpellino, L.  
Immunogenetics 34, 57-59, 1991  
A;Title: Nonobese diabetic and nonobese nondiabetic mice have unique MHC class II haplotypes  
A;Reference number: I48224; MUID:91310089; PMID:1855817  
A;Accession: I48421  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-254 <RES>  
A;Cross-references: UNIPROT:P23150; EMBL:X52643; NID:G51526; PIDN:CAA36865.1; PID:G51527  
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C;Keywords: heterodimer  
F;125-190/Domain: immunoglobulin homology <IMM>

Alignment Scores:  
Pred. No.: 4.96e-66 Length: 254  
Score: 1057.00 Matches: 198  
Percent Similarity: 93.52% Conservative: 4  
Best Local Similarity: 91.67% Mismatches: 14  
Query Match: 39.22% Indels: 0  
DB: 2 Gaps: 0

US-10-048-116-1 (1-1484) x S11649 (1-254)

QY 10 AGCAGAGCTCTGATTCTGGGGTCTCGCCTGAACACCATGCTCAGCCTCTCGGAGGT 69  
Db 2 SerArgAlaLeuLeuGlyValLeuAlaLeuThrThrMetLeuSerLeuCysGly 21  
QY 70 GAAGACGACATTGAGCGCGACCGTAGGCTTCTATGGTACAACTGTTTATCAGTCTCT 129  
Db 22 GluAspAspIleGluAlaAspHisValAlaPheTyrGlyIleSerValTyrGlnSerPro 41  
QY 130 GGAGACATTGGCCAGTACACACATGAATTTGATGGTATGAGTCTTCTATGGACTTG 189  
Db 42 GlyAspIleGlyGlnTyrThrPheGluPheAspGlyAspGluLeuPheTyrValAspLeu 61  
QY 190 GATAAGAAAGAACTCTGGAGGCTTCTGAGTTTGGCCAAATTGATCTTTTGAGCCC 249  
Db 62 AspLysGlyGlnThrValTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspPro 81  
QY 250 CAAAGTGGAGTGCAGAAATAGCTGCAGAAAAACAACTTGGGAATCTTGAACAGAGG 309  
Db 82 GlnGlyGlyLeuGlnGluIleAlaThrGlyLysTyrAsnLeuGluIleLeuIleLysAsp 101  
QY 310 TCAAAATTCACCCAGTACCAATGAGGCTCTCAAGCGACTGTGTTCCCAAGTCCCT 369  
Db 102 SerAsnPheThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 121  
QY 370 GTGCTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGACAACTTTCCACCTGTG 429  
Db 122 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProProVal 141  
QY 430 ATCAACATCAGATGGCTCAGAAATAGCAAGTCAGTCAAGCGCGGTTTATGAGACCAG 489  
Db 142 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer 161  
QY 490 TTCCTCGTCAACGTCAGCAATCTTCCACAGCTGCTTATCTCAGCTTCATCCCTCTCT 549  
Db 162 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer 181  
QY 550 GATGATGACATTTATGACTCAAGGTGAGCACTGGGGCTGGAGGAGCGGTTCTGAAA 609  
Db 182 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 201  
QY 610 CACTGGGAACCTGAGATTCCAGCCCCCATGTCAGAGCTGACAGAACT 657  
Db 202 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 217

RESULT 9  
G2MSAB  
Ig gamma-2a chain C region, secreted form (allele b) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Apr-1982 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004  
C;Accession: A02153; A32656  
R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981  
A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and IgG2b heavy chain C regions  
A;Reference number: A02153; MUID:82037861; PMID:6170065  
A;Accession: A02153  
A;Molecule type: mRNA  
A;Residues: 1-335 <SCH>  
A;Cross-references: UNIPROT:P01864; GB:J00479  
A;Experimental source: strain C57BL/6  
R;Dognin, M.J.; Lauwereys, M.; Stroobert, A.D.  
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981  
A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain C region  
A;Reference number: A32656; MUID:82037777; PMID:6794027  
A;Accession: A32656  
A;Molecule type: protein  
A;Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>  
C;Comment: Lys-335 is removed posttranslationally.  
C;Comment: The sequence differs from that of the allele, from BALB/c mice, at 15% of the chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into Ia; C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: alternative splicing; duplication; heterotetramer; glycoprotein; heterotetramer; immunoglobulin  
F;20-84/Domain: immunoglobulin homology <IM1>  
F;98-118/Region: Hinge  
F;142-311/Domain: immunoglobulin homology <IM2>  
F;142-311/Domain: immunoglobulin homology <IM3>  
F;248-315/Domain: immunoglobulin homology <IM3>  
F;15/Disulfide bonds: interchain (to light chain) #status predicted  
F;27-82,149-209,255-313/Disulfide bonds: #status predicted  
F;108,117/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 1,26e-64 Length: 335  
Score: 1037.00 Matches: 217  
Percent Similarity: 63.98% Conservative: 37  
Best Local Similarity: 54.66% Mismatches: 69  
Query Match: 38.48% Indels: 74  
DB: 1 Gaps: 9

US-10-048-116-1 (1-1484) x G2MSAB (1-335)

```
Qy 325 GCTACCAATAGGCTCTCAAGCAGCTGTGTTCCCAAGTCCCTGTG-----CTG 375
Db 1 AlalysThrThrAlaPro-----SerValTyrProLeuValProValCysGlyThr 18
Qy 376 CTGGTCAGCCACACCCCTTATCTGCTTGTGGACACATCTTCCACCTGTGATCAAC 435
Db 19 ThrGlySerSerValThrLeuGlyCysLeuVallysGlyTyrPheProGluProValThr 38
Qy 436 ATCACTAGGCTCAGAAATAGCAAGTCTCAGACACGGCGTTTATGAGACAGCTTCTC 495
Db 39 LeuThrTrp-----AsnSerGlySerLeuSerSerGlyValHis-----ThrPhePro 54
Qy 496 GTCAACCGTGACCAATCTCTCCCAAGCTGTCTTATCTCACCTTCACCTTCCTGTGAT--- 552
Db 55 AlaLeuLeuGlnSerGlyLeuTyrThrLeuSerSerSerValThrValThrSerAsnThr 74
Qy 553 -----GATGACATTTATGACTGCAAGTGGAGACTGGGGCCTGGAGGACCCGGTCTG 606
Db 75 TrpProSerGlnThrIleThrCysAsnValAlaHis----- 86
Qy 607 AAACACTGGGAACCTGAGATTCCAGCCCCCATGTTCAGAGCTGCAGAGAACTGGAGTGA 666
Db 86 ----- 86
Qy 667 GGATCCACTACAGCTCCATCAGCTCAGCTCGAAAGAGCTCCAGGCCCTGGAGAGGAA 726
Db 87 -----ProAlaSerSerThrLysValAspLysLysIle----- 97
Qy 727 AATGCACAGCTGGGAATGGAGTTCCAGCACTGGAAAGGAACCTGGCTCAGGCAGCATCT 786
Db 97 ----- 97
Qy 787 GAGCCCAAGAGGCCCC---ACAATCAAGCCCTGTCTCCATGCMAA-----TGC 831
Db 98 GluProArgValProIleThrGlnAsnProCysProProHisGlnArgValProCys 117
Qy 832 CCAGCACTAACCTCTTGGGTGGACCAATCCGCTTCATCTTCCCTCCAAAGATCAAGAT 891
Db 118 AlaAlaProAspLeuLeuGlyGlyProSerValPheIlePheProProLysIleLysAsp 137
Qy 892 GTACTCATGATCTCCCTGAGCCCATAGTACATGTGTGGTGGTGGATGTGAGCGAGAT 951
Db 138 ValLeuMetIleSerLeuSerProMetValThrCysValValValAspValSerGluAsp 157
Qy 952 GACCCAGATGTCCAGATCAGCTGTGTTGTGAACACCTGGAAGTACACAGCTTCAGACA 1011
Db 158 AspProAspValGlnIleSerTrpPheValAsnAsnValGluValHisThrAlaGlnThr 177
Qy 1012 CAACCCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTCACTGCCCTCCCATCCAG 1071
Db 178 GlnThrHisArgGluAspTyrAsnSerThrLeuArgValValSerAlaLeuProIleGln 197
Qy 1072 CACCAGGACTGGATGGGCAAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCCA 1131
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Db 198 HisGlnAspTrpMetSerGlyLysGluPheLysCysLysValAsnAsnArgAlaLeuPro 217
Qy 1132 GCGCCCATCAGAGAAACCATCTCAAAACCCAAAGGGTCAGTAAGAGTCCACAGGTATAT 1191
Db 218 SerProIleGluLysThrIleSerLysProArgGlyProValArgAlaProGlnValTyr 237
Qy 1192 GTCTTGCTCTCACCAGAAAGAGATGACTAAGAAACAGAGTCACTCTGAGCTGATGGTC 1251
Db 238 ValLeuProProAlaGluMetThrLysLysGluPheSerLeuThrCysMetIle 257
Qy 1252 ACAGACTTTCATGCTGAAGACATTTAGCTGAGTGGACCAACACGGGAAACAGAGCTA 1311
Db 258 ThrGlyPheLeuProAlaGluIleAlaValAspTrpThrSerAsnGlyArgThrGluGln 277
Qy 1312 AACTTACAAGAACACTGAACAGCTCCTGGACTCTGTATGGTCTTCTTACTTTCATGTACAGCAAG 1371
Db 278 AsnTyrLysAsnThrAlaThrValLeuAspSerAspGlySerTyrPheMetTyrSerLys 297
Qy 1372 CTGAGAGTGGAAAGAAAGAACTGGGTGGAAAGAAATAGTACTCTCTTCTGAGTGGTCCAC 1431
Db 298 LeuArgValGlnLysSerThrTrpGluArgGlySerLeuPheAlaCysSerValValHis 317
Qy 1432 GAGGCTCTGCACAAATCACCACAGCTAAGAGCTTCTCCCGGACTCCCGGT 1482
Db 318 GluValLeuHisAsnHisLeuThrThrLysThrIleSerArgSerLeuGly 334

RESULT 10
G2MSBM
Ig gamma-2b chain C region, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: C02154; A02158; B02157
R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul
A;Reference number: A02154; MUID:82222190; PMID:6283537
A;Accession: C02154
A;Molecule type: DNA
A;Residues: 335-405 <YAM>
A;Cross-references: UNIPROT:P01867; GB:J00462
R;Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma c
A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: A02158
A;Molecule type: DNA
A;Residues: 335-378 <ROG>
A;Note: the translation of the first exon of the membrane-bound segment is given
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from n
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: B02157
A;Molecule type: DNA
A;Residues: 1-335, 'K' <YA2>
C;Comment: The sequence of residues 1-334 was assumed to be identical with the correspon
C;Comment: Cell lines producing IGG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C;Genetics:
A;Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;143-212/Domain: immunoglobulin homology <IMW>
F;352-369/Domain: intracellular #status predicted <TMW>
F;370-405/Domain: intracellular #status predicted <INT>
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 6.58e-63 Length: 405
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Score: 1012.50 Matches: 210  
Percent Similarity: 63.59% Conservative: 38  
Best Local Similarity: 53.85% Mismatches: 69  
Query Match: 37.57% Indels: 73  
DB: 1 Gaps: 10

US-10-048-116-1 (1-1484) x G2MSB (1-405)

QY 349 ACTGTGTTCCCAAGTCCCT-----GTGCTGCTGGTGCAGCCCAACACCCCTTATC 399  
Db 7 SerValTyrProLeuAlaProGlyCysGlyAspThrThrGlySerSerValThrLeuGly 26  
QY 400 TGTCTTTGGACAACTTTCACCTGTGATCAACATCATCATGGCTGAGAATAGCAAG 459  
Db 27 CysLeuValLysGlyTyrPheProGluSerValThrValThrTrp-----AsnSerGly 44  
QY 460 TCAGTCACAGACGGCTTTATGAGACGACGCTTCTGTCACCGTGCACCATCTCTCCAC 519  
Db 45 SerLeuSerSerSerValHis-----ThrPheProAlaLeuLeuGlnSerGlyLeuTyr 62  
QY 520 AAGCTGCTTATCTCACCTTCATCTCTCTGAT-----GATGACATTTATGACTGC 570  
Db 63 ThrMetSerSerSerValThrValProSerSerThrTrpProSerGlnThrValThrCys 82  
QY 571 AAGGTGGACACTGGGGCCCTGGAGGAGCCGGTTCTCAAAACACTGGGAACCTGAGATTCA 630  
Db 83 SerValAlaHis-----Pro 87  
QY 631 GCCCCATGTACAGCTGACAGAACTGGAGTGGAGATCCACTACAGCTCCATCAGCT 690  
Db 88 Ala-----SerSerThrThr 92  
QY 691 CAGCTCGAAAAAGAGCTCCAGGCCCTGGAGAGGAAAAATGCACAGCTGGAATGGAGTTG 750  
Db 92 ----- 92  
QY 751 CAAGCACTGGAAGAAGAACTGGCTCAGGCAGCATCTGAGCCCGAGGGGCC-----ACA 804  
Db 93 -----ValAspLysLysLeu-----GluProSerGlyProLysSerThr 105  
QY 805 ATCAAGCCCTGCTCTCATGC-----AAATGCCAGCAGCTTAACCTCTTGGGT 852  
Db 106 IleAsnProCysProCysLysGluCysHisLysCysProAlaProAsnLeuGluGly 125  
QY 853 GGACCATCGCTCTTCTATCTTCCCTCAAGATCAAGATGATCTCATGATCTCCCTGAGC 912  
Db 126 GlyProSerValPheLeuPheProProAsnLysAspValLeuMetLysLeuThr 145  
QY 913 CCATAGTCATGTGTGGTGGTGGATGTGAGGAGGATGACCCAGATGTCCAGATCAGC 972  
Db 146 ProLysValThrCysValValValAspValSerGluAspAspProAspValGlnLysSer 165  
QY 973 TGTGTTGTGAACAGCTGGAGTACACAGCTCAGACACAAACCATAGAGGATTAC 1032  
Db 166 TrpPheValAsnAsnValGluValHisThrAlaGlnThrGlnThrHisArgGluAspTyr 185  
QY 1033 AACAGTACTCTCCGGTGGTGCAGTCCCTCCCATCCAGCAGCAGCTGGATGAGTGC 1092  
Db 186 AsnSerThrLeuValSerValSerThrLeuProLysGlnHisGlnAspTrpMetSerGly 205  
QY 1093 AAGGAGTTCAAATGCAAGGTCAACAAAGACCTCCAGCGCCCATCCAGAGAACCATC 1152  
Db 206 LysGluPheLysCysLysValAsnAsnLysAspLeuProSerProLysGluArgThrLe 225  
QY 1153 TCAAAACCCAAAGGTCAGTAAGAGCTCCAGGATATGTCTTGGCTCCACCAAGAA 1212  
Db 226 SerLysIleLysGlyLeuValArgAlaProGlnValTyrIleLeuProProAlaGlu 245  
QY 1213 GAGATGACTAAGAAACAGCTCACTCTGACCTGCTGATGTCACAGCTTCATGCTGAAC 1272  
Db 246 GlnLeuSerArgLysAspValSerLeuThrCysLeuValValGlyPheAsnProGlyAsp 265  
QY 1273 ATTTACGTGGAGTGACCAACACGGGAAAAACAGAGCTAAACTTACAAGAACTGAACCA 1332

Db 266 IleSerValGluTrpThrSerAsnGlyHisThrGluAsnTyrLysAspThrAlaPro 285  
QY 1333 GTCTGGACTCGATGGTTCTTACTTCATGTCAGCAGCAAGCTGAGATGGGAAAGAGAAC 1392  
Db 286 ValLeuAspSerAspGlySerTyrPheIleTyrSerLysLeuAsnMetLysThrSerLys 305  
QY 1393 TGGGTGGAAAGAAATAGTACTCTCTGTCAGTGGTCCAGAGGCTTCGACAAATCACCAC 1452  
Db 306 TrpGluLysThrAspSerPheSerCysAsnValArgHisGluGlyLeuLysAsnTyrTyr 325  
QY 1453 AGCACTAAGAGCTTCTCCCGGACTCCGGGT 1482  
Db 326 LeuLysLysThrIleSerArgSerProGly 335

RESULT 11  
G2MS11  
IG gamma-2b chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004  
C:Accession: S25057; A02157; A26235; A26233; A53598  
R:Fischer, R.; Voss, A.; Nierebach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
submitted to the EMBL Data Library, July 1992  
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m  
A:Reference number: S25057  
A:Accession: S25057  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-474 <FIS>  
A:Cross-references: UNIPROT:P01866; EMBL:X67210; NID:G54826; PIDN:CAA47649.1; PID:G54827  
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from ne  
A:Reference number: A02157; MUID:80120716; PMID:6766534  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', '163-189', 'FP', '193-474' <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A:Reference number: A26235; MUID:80081501; PMID:117548  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', '174-189', 'FP', '193-376', 'T', '378-474' <TUI>  
A:Note: Lys-474 is probably removed posttranslationally  
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A:Reference number: A26233; MUID:80081502; PMID:117549  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', '174-189', 'FP', '193-376', 'T', '378-474' <TUI>  
R:Ollo, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma  
A:Reference number: A26233; MUID:82173203; PMID:6803173  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', '163-189', 'FP', '193-300', 'R', '302-331', 'A', '333-437', 'DI', '440-474' <OLL>  
A:Cross-references: GB:J00461  
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359; PMID:7512967  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <KIM>

C;Comment: The a allele sequence is shown.

C;Genetics: 138/1; 236/1; 258/1; 368/1  
 A;Introns: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes: immunoglobulin C region; immunoglobulin homology  
 C;Superfamily: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
 C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;236-257/Region: hinge  
 F;281-350/Domain: immunoglobulin homology <IM2>  
 F;387-454/Domain: immunoglobulin homology <IM3>  
 F;152/Disulfide bonds: interchain (to light chain) #status predicted  
 F;164-220,288-348,394-452/Disulfide bonds: #status predicted  
 F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted  
 F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:  
 Pred. No.: 9,97e-63 Length: 474  
 Score: 1010.00 Matches: 217  
 Percent Similarity: 60.99% Conservativity: 41  
 Best Local Similarity: 51.30% Mismatches: 75  
 Query Match: 37.48% Indels: 90  
 DB: 1 Gaps: 12

US-10-048-116-1 (1-1484) x G2MS11 (1-474)

Qy 250 CAAGTGAGCTGCAAAACATAGCTGCGAGAAAACACAACTTGGGAATCTTGACTAAGAGG 309  
 Db 129 GlnGlyThrLeuValThrValSerAlaAlaLys 139  
 Qy 310 TCAAAATTTCAACCCAGCTACCAATGAGCTCTCTCAAGCGACTGTGTTCCCAAGTCCCT 369  
 Db 140 -----ThrThrPro-----ProSerValThrProLeuAlaPro 150  
 Qy 370 -----GTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420  
 Db 151 GlyCysGlyAepThrThrGlySerSerValThrSerGlyCysLeuValLysGlyTyPhe 170  
 Qy 421 CCACCTGTGATCAACATCAGATGCTCAGAAATAGCAAGTCAAGTCAAGCGGGTTAT 480  
 Db 171 ProGluSerValThrValThrTrp-----AsnSerGlySerLeuSerSerValHis 188  
 Qy 481 GAGACCACTCTCTCGTCAACCGTCCATCTCTCCACAGCTGCTTATCTCACCTTC 540  
 Db 189 ThrLeuSerGlnAlaLeuGlnSerGlyLeuTyThrMetSerSerValThr--- 207  
 Qy 541 ATCCCTCTCTGAT-----GATGACATTTATGACTGCAAGGTGGAGCACTGGGGCTG 591  
 Db 208 ValProSerSerThrTrpProSerGlnThrValThrCysSerValAlaHis----- 224  
 Qy 592 GAGGAGCGGTCTGAAACACTGGGAACCTGAGATTCCAGCCGCCATGTGACGCTGACA 651  
 Db 225 -----ProAla----- 226  
 Qy 652 GAAACTGGAGTGGAGGATCCACTACAGCTCCATCAGCTCAGCTCGAAGAAAGACTCCAG 711  
 Db 227 -----SerSerThr----- 230  
 Qy 712 GCCCTGGAGAGGAAAATGCACAGCTGGAATGGGAGTTGCAAGCACTGGAAAAGAACTG 771  
 Db 231 -----ValAspLysLysLeu 235  
 Qy 772 GCTCAGCAGCATCTGAGCCAGAGGGGCC-----ACAATCAGCCCTGCTCTCCATGC 825  
 Db 236 -----GluProSerGlyProLeuSerThrLeuAsnProCysProCys 250  
 Qy 826 -----AAATGCCAGCACCTTAACCTCTGGGTGGACCATCCGCTCTTCATCTTC 873  
 Db 251 LysGluCysHisLysCysProAlaProAsnLeuGluGlyGlyProSerValPhePhe 270  
 Qy 874 CCTCAAGATCAAGGATGACTCATGATCTCTGAGCCCCCAATGATGATGCTG 933  
 Db 271 ProProAsnLysAspValMetLeuSerLeuThrProLysValThrCysValVal 290

Qy 934 GTGGATGTGAGCCAGGATGACCCAGATGTCAGATCAGCTGCTTCTGAACAACTGGAA 993  
 Db 291 ValAspValSerGluAepAspProAspValGlnIleSerTrpPheValAsnValGlu 310  
 Qy 994 GTACACACAGCTCAGACACAAACCCATAGAGAGATTACAACTACTCTCCGGGTGTC 1053  
 Db 311 ValHisThrAlaGlnThrGlnThrHisArgGluAspTyrAsnSerThrIleArgValVal 330  
 Qy 1054 AGTGCCCTCCCATCCAGCACCAAGGACTGGATGATGCGCAAGGAGTTCAAATGCAAGTTC 1113  
 Db 331 SerThrLeuProIleGlnHisGlnAspTrpMetSerGlyLysGluPheLysCysLysVal 350  
 Qy 1114 AACAAACAAACCTCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGTCAGTA 1173  
 Db 351 AsnAsnLysAspLeuProSerProIleGluArgThrIleSerLysIleLysGlyLeuVal 370  
 Qy 1174 AGAGCTCCACAGGTATATGTTCTTCCTCCACCAAGAGAGATGACTTAAGAAACAGTTC 1233  
 Db 371 ArgAlaProGlnValTyrIleLeuProProAlaGlnLeuSerArgLysAspVal 390  
 Qy 1234 ACTCTGACCTGCATGCTCAGAGCTTCATCGCTGAAAGACATTTACGTGGAGTGGACCAAC 1293  
 Db 391 SerLeuThrCysLeuValValGlyPheAsnProGlyAspIleSerValGluTrpTrpSer 410  
 Qy 1294 AACGGGAAAACAGAGCTAAACTACAGAACACTGAACCACTCTGGAGCTCTGATGCTTCT 1353  
 Db 411 AsnGlyHisThrGluGluAsnTyrLysAspThrAlaProValLeuAspSerAspGlySer 430  
 Qy 1354 TACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAAGAACTGGGTGGAAAGAAATAGCTAC 1413  
 Db 431 TyrPheIleTyrSerLysLeuAsnMetLysThrSerLysTrpGluLysThrAspSerPhe 450  
 Qy 1414 TCCTGTTTCACTGCTCCAGAGGCTGTCACAACTCACACAGCACTTAAGAGCTTCTCCCGG 1473  
 Db 451 SerCysAsnValArgHisGluGlyLeuLysAsnTyrTyrLeuLysLysThrIleSerArg 470  
 Qy 1474 ACTCCGGGT 1482  
 Db 471 SerProGly 473  
 RESULT 12  
 S01321  
 Ig gamma-2b chain precursor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
 C;Accession: S01321  
 Eur. J. Biochem. 176, 287-295, 1988  
 A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a  
 A;Reference number: S01320; MUID:88329081; PMID:3138116  
 A;Accession: S01321  
 A;Molecule type: mRNA  
 A;Residues: 1-475 <DE1>  
 A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781  
 A;Note: this sequence was determined from the differentiated gene  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: immunoglobulin  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
 F;159-223/Domain: immunoglobulin homology <IMV>  
 Alignment Scores:  
 Pred. No.: 1.9e-62 Length: 475  
 Score: 1006.00 Matches: 214  
 Percent Similarity: 62.28% Conservativity: 37  
 Best Local Similarity: 53.10% Mismatches: 76  
 Query Match: 37.33% Indels: 76  
 DB: 2 Gaps: 11  
 US-10-048-116-1 (1-1484) x S01321 (1-475)  
 Qy 319 ACCCCAGCTACCAATGAGGCTCCTCAAGCAGCT-----GTGTTCCCAAGTCCCT 369



Db 161 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 180

Qy 610 CACTGGGAACCTGAGATTCCAGCCCCATGTGACAGCTGACAGAAACT 657  
|||||  
Db 181 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 196

RESULT 14

179358

IA-alpha polypeptide - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I79358  
R;Landais, D.; Matthes, H.; Benoist, C.O.; Mathis, D.  
Proc. Natl. Acad. Sci. U.S.A. 82, 2930-2934, 1985  
A;Title: A molecular basis for the Ia.2 and Ia.19 antigenic determinants.  
A;Reference number: 159023; MUID:85190610; PMID:2581258  
A;Accession: I79358  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: UNIPROT:P14437; GB:M11358; NID:g199465; PIDN:AAA39622.1; PID:g387462  
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C;Keywords: polyprotein  
F;104-169/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	8.89e-62	Length:	233
Score:	996.00	Matches:	183
Percent Similarity:	95.41%	Conservative:	4
Best Local Similarity:	93.37%	Mismatches:	9
Query Match:	36.96%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116-1 (1-1484) x I79358 (1-233)

Qy 70 GAAGACGACATTGAGCGGCACAGTGGCTTCTATGGTACAACTGTTTATCAGTCTCCT 129  
|||||  
Db 1 GluAspAspIleGluAlaAspHisValGlyValTyrGlyThrValTyrGlnSerPro 20

Qy 130 GGAGACATTGCCAGTACACATGAATTTGATGGTGAATGTTGTTCTATGTGGACTTG 189  
|||||  
Db 21 GlyAspIleGlyGlnTyrThrHisGluPheAspGlyAspGluTyrPheTyrValAspLeu 40

Qy 190 GATAGAGAAAATGCTGAGGCTTCTGAGTTGGCCAAATGATCTTTTGAGCCC 249  
|||||  
Db 41 AspLysLysGluThrIleTrpMetLeuProGluPheGlyGlnLeuThrSerPheAspPro 60

Qy 250 CAAGGTGACTGCAAAACATAGCTGCAGAAAAACAACTTGGGAATCTTGACTAAGAGG 309  
|||||  
Db 61 GlnGlyLeuGlnAsnIleAlaThrGlyLysTyrThrLeuGlyIleLeuThrLysArg 80

Qy 310 TCAAAATTTCAACCGTACCAATCCATGAGCTCCTCAAGGACTGTGTTCCCAAGTCCCT 369  
|||||  
Db 81 SerAsnSerThrProAlaThrAsnGluAlaProGlnAlaThrValPheProLysSerPro 100

Qy 370 GTGCTGTGGGTGAGCCCAACACCTTATCTGCTTGTGGACACATCTTCCACCTGTG 429  
|||||  
Db 101 ValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePheProVal 120

Qy 430 ATCAACATCATATGGCTCAGAAATAGCAAGTCAAGTCAAGCGCGGTTTATGAGACGAGC 489  
|||||  
Db 121 IleAsnIleThrTrpLeuArgAsnSerLysSerValThrAspGlyValTyrGluThrSer 140

Qy 490 TTCCTCGTCAACCGTGACCATCTTCCACAAAGCTGTCTATCTCACTTCACTCCCTTCT 549  
|||||  
Db 141 PheLeuValAsnArgAspHisSerPheHisLysLeuSerTyrLeuThrPheIleProSer 160

Qy 550 GATGATGACATTTATGACTGAAGTGGAGCACTGGGGCCGTGGAGCGGTTCTGAAA 609  
|||||  
Db 161 AspAspAspIleTyrAspCysLysValGluHisTrpGlyLeuGluProValLeuLys 180

Qy 610 CACTGGGAACCTGAGATTCCAGCCCCCATGTGACAGCTGACAGAAACT 657  
|||||

Db 181 HisTrpGluProGluIleProAlaProMetSerGluLeuThrGluThr 196

RESULT 15

S02855

class II histocompatibility antigen RT1-B(b) alpha chain precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: S02855  
R;Barran, P.A.; McMaster, W.R.  
Immunogenetics 26, 56-62, 1987  
A;Title: DNA sequence analysis of the rat RT1-B-alpha gene.  
A;Reference number: S02855; MUID:87278361; PMID:3610254  
A;Accession: S02855  
A;Molecule type: DNA  
A;Residues: 1-256 <BAR>  
A;Cross-references: UNIPROT:P20037; EMBL:X07550  
C;Genetics:  
A;Introns: 29/1; 112/1; 206/1  
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;24-256/Product: class II histocompatibility antigen, RT1-B(b) alpha chain #status pred  
F;127-192/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.:	4.24e-60	Length:	256
Score:	972.00	Matches:	179
Percent Similarity:	89.04%	Conservative:	16
Best Local Similarity:	81.74%	Mismatches:	24
Query Match:	36.07%	Indels:	0
DB:	2	Gaps:	0

US-10-048-116-1 (1-1484) x S02855 (1-256)

Qy 1 ATGCGCTGCAGCAGACTCTGATTCTGGGGTCTCCGCCCTCAACACACATCTCAGCCTC 60  
|||||  
Db 1 MetProLeuSerArgAlaLeuIleLeuGlyValLeuAlaLeuThrMetLeuSerPro 20

Qy 61 TGGGAGGTGAAGACGACATTGAGCGCGACAGTAGGCTTCTATGTGTACAACTGTTTAT 120  
|||||  
Db 21 CysGlyGlyGlnAspAspIleGluAlaAspHisValGlySerTyrGlyIleThrValTyr 40

Qy 121 CAGTCTCTCGACACATTGGCCAGTACACATCAATTCATGCTGATGATGTTCTCTAT 180  
|||||  
Db 41 GlnTyrHisGluSerLysGlyGlnTyrThrHisGluPheAspGlyAspGluArgPheTyr 60

Qy 181 GTGACTTGGATGAAGAGAAAATGCTGAGGCTTCTGAGGCTTCTGAGTTTGGCCAAATTCATC 240  
|||||  
Db 61 ValAspLeuAspLysLysGluThrIleTrpArgIleProGluPheGlyGlnLeuIleSer 80

Qy 241 TTTGAGCCCAAGGTGACATGCAAAACATAGCTGCAGAAACACAACTTGGGAATCTTG 300  
|||||  
Db 81 PheAspProGlnGlyAlaLeuArgAsnIleAlaIleIleLysHisAsnLeuGluIleLeu 100

Qy 301 ACTAAGAGGTCAAAATTTCCGCCAGCTACCAATGAGGCTCTCAAGCGACTGTCTCCCC 360  
|||||  
Db 101 MetLysArgSerAsnSerThrProAlaValAsnGluValProGluAlaThrValPheSer 120

Qy 361 AAGTCCCTCTGTGCTGGGTGAGCCCAACACCTTATCTGCTTTGTGGCAACATCTTC 420  
|||||  
Db 121 LysSerProValLeuLeuGlyGlnProAsnThrLeuIleCysPheValAspAsnIlePhe 140

Qy 421 CCACCTGTGATCAACATCATCATGGCTCAGAAATAGCAAGTCAGTCACAGCGGGTTTAT 480  
|||||  
Db 141 ProProValIleAsnIleThrTrpLeuArgAsnSerLysProLeuThrGluGlyValTyr 160

Qy 481 GAGACACAGTCTCTCGTCAACCGTACCATTTCTTCCACAAGCTGTCTTATCTCACCTTC 540  
|||||  
Db 161 GluThrSerPheLeuIleAsnSerAspTyrSerPheHisLysMetAlaTyrLeuThrPhe 180

Qy 541 ATCCCTTCTGATGATGACATTTTATGACTGCAAGGTGGAGCACTGGGGCCCTGGAGAGCCG 600  
|||||  
Db 181 IleProSerAsnAspAspIleTyrAspCysLysValGluHisTrpSerLeuAspGluPro 200





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